Mq

From:

Marvich, Maria

Sent:

Tuesday, November 01, 2005 6:33 AM

To: Subject:

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368--1144 of SEQ ID NO:34

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Maria Bonovich Marvich, PhD

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Date completed:
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Online Time:

Type of Search

NA#______ AA#:_____

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Inventor:_____ Litigation:_____

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SEQUENCE SYSTEM:
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Other (Specify):

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AY389535 Mus muscu AY38954 Mus muscu AY13898 Oryctolag AY144238 Sus scrof AZ288373 Bos tauru AA006756 Sus scrof AC12242 Atelerix BX088554 Zebrafish AC119375 Rattus no AC119375 Rattus no AC119375 Rattus no AC119376 Homo sapi AX430407 Sequence AL591378 Homo sapi BX64751 Danio rer CR388410 Danio rer AL590243 Human DNA AL156513 Human DNA

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597 bp DNA linear PRI 03-MAY-1999 isoform 2, promoter and 5'UTR sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
.. (bases 1 to 59)
.. Auboeuf, D., Raspe, B., Schoonjans, K., Lefebvre, A.-M., Saladin, R., Najib, J., Laville, M., Fruchart, J.-C., Deeb, S., Puig-Vidal, A., Flier, J., Briggs, M., Vidal, H., Staels, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-JUL-1997) Cardiovascular Res., Ligand Pharmaceuticals, 9393 Towne Centre Dr., San Diego, CA 92121-3016, USA
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J. Biol. Chem. 272 (30), 18779-18789 (1997)
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Direct Submission
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AV389534
AC131898
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AC19375
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464. .597
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/note="isoform 2"
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40.3 13003
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29.2 1077
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9.4 166854
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AX755166 Sequence
AC03174 Homo sapi
AX157024 Homo sapi
AC151849 Callithri
AC136055 Rattus no
AC136055 Rattus no
AC136056 Rattus no
S79407 mPPAR gamma
AX24364 Mus muscu
AC125447 Mus muscu
AC125417 Mus muscu
AC125531 Mus muscu
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                 5.1.6
Compugen Ltd.
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                   GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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MCKay,R., Borchers,A.H. and Baker,B.F.
Antisense modulation of peroxisome proliferator-activated receptor
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        /codon_start=1
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Pred. No. 7.3e-97;
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Pred. No. 7.4e-97;
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Sequence 10 from patent US 6159734..
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Patent: US 6159734-A 10 12-DEC-2000;
Location/Qualifiers
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Lim,C.H., Kok,C.C., Samian,M.R., Najimudin,N. and Tengku Muhammad,T.S.
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Submitted (03-OCT-2000) School of Biological Sciences, Universiti
Sains Malayala, Minden, Penang 11800, Malaysia
Location/Qualifiers
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                                                                                   CAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGAATTCCAAATTTTTC
                                                                 31 CAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGAATTCCAAAATTTTTC
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Lim,C.H., Kok,C.C., Samian,M.R., Najimudin,N. and Tengku Muhammad,T.S.
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   Length 597;
Query Match 94.0%; Score 473; DB 9; Length 59 Best Local Similarity 100.0%; Pred. No. Se-101; Matches 473; Conservative 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                 /product="peroxisome proliferator activated-receptor
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                                                                                                                                                                                                         Score 455.2; DB 9; Length 1100;
Pred. No. 7.3e-97;
0; Mismatches 8; Indels 8;
                                                                                 /protein_id="BAA23353.1"
/db_xref="G1:2605489"
/tramalation="MGFTLGDSPIDPESDSFTDTLSANISQ"
/gene="ppar gamma2"
               'note="ppar gamma2 specific coding region"
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Patent: WO 03093310-A 3 13-NOV-2003;
Universitaet Bremen (DE)
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Sequence 3 from Patent W003093310.
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1. .85873
/organism="Homo sapiens"
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gene="ppar gamma2"
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                                 /codon start=1
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/tigsue type="placenta"
859. 940
/gene="ppar gamma2"
859. >940
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Submitted (13-AUG-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
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96.8%; Pred. No. 4.5e-97;
iive 0; Mismatches 8;
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/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-167M22"
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/organism="Homo sapiens"
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Center code:Beijing Center
Center code:Beijing
Website:http://hgc.igtp.ac.cn
http://www.genomice.org.cn
Contact:hgc@igtp.ac.cn
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Best Local Similarity 96.8
Matches 488; Conservative
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Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
                                                                                                                                                                                                                                                         61 AIGGATACATATTIGAATTICCAAATTTTTCTTCAGATAATGIGATTAGAGATTAGAGATT 120
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                                                                                                                                                                         1 TAGAGTAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACT
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                                                                                          DB 6; Length 85873;
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Homo sapiens chromosome 3 clone RP11-167M22 map 3p,
sequence.
                                                                                                                                   Indels
                                                                                                                                     8
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Pred. No. 4.7e-97;
0; Mismatches 8
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Homo sapiens
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06715. .106853,119980. .120179,130803. .131253,
47997. .148443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="PPARG"
product="peroxisome proliferative activated receptor
                                                                                                                                                                                                                                                                                                    754. .1925
note="Region not scanned for variation"
784. .2127
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 148828)
Rieder, M.J., da Ponte, S.H., Kuldanek, S.A., Rajkumar, N., Smith, J.D., Toth, E.J. and Nickerson, D.A.
Direct Submission
Submitted (30-SEP-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
                                                                                                                                           300
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CAACCAGGGATAGACACCGAAAAGTTTGCCCCAAATAAGCTTTCTGGTATTTCATAA 180
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Ahearn,M.O., Rajkumar,N., Yi,Q. and Nickerson,D.A.
Direct Submission

Submitted (16-UNN-2004) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA

1705 NE Pacific, Seattle, WA 98195, USA

On Jun 16, 2004 this sequence version replaced gi:23953882.

To cite this work please use: SeattleSNPs. NHLBI Program for Genomic Applications, UW-FRCRC, Seattle, WA

(URL:http://pga.mbt.weshington.edu).
                      81311 CAACCAGGAATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA
                                                                                                     31371 GCAAGAGATTTAAGTTTTTCCATTTAAGAAGCAATTGTGAATTTTACAACAATAAAAATG
                                                                     GCAAGAGATTTTAAGTTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATG
                                                                                                                                         241 CAAGTGGATATTGAACAGTCTCTTCTTGATAATTCTAAATACAGTACAGTTCACGCCCC
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1 (Bases I to 166049)

Wu, Q. Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, Y., Li, W., Sun, W., Sun, Y., Tao, R., Wang, H., Wang, J.,
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                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                      Query Match 90.5%; Score 455.2; DB 9; Length 148828; Best Local Similarity 96.8%; Pred. No. 4.4e-97; Matches 488; Conservative 0; Mismatches 9; Indels 8;
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AC090847 AC016333
AC090847.2 G1:24796728
HOMO sapiens (human)
Homo sapiens (human)
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                                                                                      "note="Region not scanned for variation"
1952. .6004
Trpt_family="MIR"
Trpt_type=dispersed
1735. .9019
                                                                                                                                                   /rpt_family="Alu"
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/rpt_family="L2"
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/rpt_family="L2"
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2949. .13255
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To bases I to 166049)

While Dang, W., Pan, H., Feng, X., Gong, J., Guan, Q., Guo, D., Guo, D., Guo, E., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, T., Li, W., Li, C., L
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Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zhang, G., Zhang, H., Zhang, H., Zhang, I., Zhang, M., Zhang, X., Zhang, Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Direct Submission

Submitted (08-NOV-2002) Human Genomic Center, Institute of Schenittes, Chinese Academy of Sciences, Datun Road, Beljing, Genetics, Chinese Academy of Sciences, Datun Road, Beljing, 100101, P.R.China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Nov 8, 2002 this sequence version replaced gi:13384351.
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator B19 Dye; 45% of reads
Assembly program: Phrap; version 0.390329
Consensus quality: 499 bases at least Q40
Consensus quality: 670 bases at least Q30
Insert size: 692; sum-of-contigs
Quality coverage: 2.80x in Q20 bases;sum-of-contigs
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Center project name:1% project
Center clone name: RP11-30G23
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/db_xref="taxon:9606"
                                                                                                                                                                                                  Chromosome 3p genomic sequence
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http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
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AUTHORS
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145789 TAGAGTAAGTACCTTAGGAATATAAACATTTCAGTAGCATGCTGATACCAACGTTTAAACT 145730
                                                                                                                                   145729 ATGGATACATATTTGAATTCCAAATTTTTCTTCAAATAATGT-----GATTAGAGATT 145677
                                                                                                                                                                                                                                                145676 CAACCAGGAATAGACACCGAAAGAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA 145617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACISIB49 186028 bp DNA linear HTG 08-OCT-2004
Callithrix jacchus clone CH259-42F14, WORKING DRAFT SEQUENCE, 2
ordered pieces.
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Submitted (08-OCT-2004) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Callithrix jacchus (whīte-tufted-ear marmoset)
Callithrix jacchus (briedata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                    145616 GCAAGAGATTTAAGTTTTCCATTTAAGAAGCAATTGTGAATTTACAACAATAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145556 CAAGTGGATATTGAACAGTCTCTGCTCTGATAATTCTAAATACAGTACAGTTACAGTTCACGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145496 TCACAAGACACTGAACATGTGGGTCACCGGCGAGACAGTGTGGCAATATTTTCCCTGTAA
                                                                                                                                                                                                        CAACCAGGGATAGACACCGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAGTGGATATTGAACAGTCTCTCTCTGATAATTCTAAATACAGTACAGTTCACGCCCC
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                                                                     ATGGATACATATTTGAATTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATT
                                                                                                                                                                                                                                                                                                                                                      181 GCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 TGTACCAAGTCTTGCCAGAGCAGTGAACATTATGACACTACTATTTTGTCACAGCTGGCTC
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1 (bases 1 to 186028)
Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R., Peng,Z., Palinov,I. and Rubin,E.M.
Direct Submission
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http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=PPARG
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Center Code: PGABERK
Center Project Name: J108-42F14
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Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 26679: contig of 26679 by in length.

* 26679: contig of 189249 bp in length.

Location/Qualifiers
                       The order-orientation of the draft sequence was accomplished by
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Avid (http://baboon.math.berkeley.edu/mavid) and paired end
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                                                                                                                                 Funding agent: Programs for Genomic Applications (NHLBI)
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                                                                                                                                                                                                                                                                                                                 (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Worley, K.C.

Direct Submission

L. Submitted (13-7002) Human Genome Sequencing Center, Department of Submitted (13-7004-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:22855703.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a caffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated aize. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome chance and the ends of the clone and sequences and whole genome chance and the ends of the clone and sequences and whole genome chance who whole genome chance will not the capture and the patter of the feature chance will not the capture capture and the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole capture and the capture capture capture will not the capture and the capture capture capture will not the capture capture capture capture will not capture will not capture will not capture capture will not capture capture will not capture will not capture will not capture capt
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* See http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* Consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
                                                                                                                                              Worley, K.C.
Direct Submission
Submitted (20-APR-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 AACTATGGATACATATTTGAATTCCAAATTTTTTTTTCTGATAATGTGATTAGAGATTAGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shotgun sequence only contigs will be indicated in the feature
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1 245724: contig of 245724 bp in length.
Location Qualifiers
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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243338. .245724
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                                                                                                                 (bases 1 to 245724)
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Best Local Similarity 75.34
Matches 342; Conservative
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SMLAN, D.M., Adman.C., Aldo-Oddola, B., All-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, J., Benten, J., Estreva, M., Brown, B., Brankshurg, K., Bonnin, D., Bouck, J., Bowle, S., Birkea, M., Brown, B., Brown, M., Bryant, N.P., Bunky, C., Burch, F., Burkett, C., Burrell, K.L., Byrd, N.C., Covlen, G., Chen, G., Chen, G., Chowdhry, I., Christopoulos, C., Covlen, G., Cox, C., Covle, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Defareich, D.A., David, R., Douthwaite, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggon, N., Ford, J., Forter, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Harr, M., Havlad, P., Hamilton, K., Hernandez, O., Hodgeon, M., Holloway, C., Hollins, B., Hernandez, O., Hodgeon, M., Holloway, C., Hollins, B., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Youda, S., Kovar, C., Karlsson, E., Kelly, S., Huber, J., Hully, S., Hume, J., Jackson, L.E., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Joudah, S., Kovar, C., Lichteargo, G., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R., Jak, Massey, B., Marting, M., Martinez, B., Massey, B., Mantiney, E., McLed, R., Marting, M., Martinez, B., Massey, B., Mantiney, E., McLed, R., Pattin, R., Martin, R., Martin, R., Massey, B., Mantin, R., Macken, M., Mei, G., Merzker, M., Mei, G., Merzker, M., Mei, G., Murt, S., Sonak, M., Stener, J., Perter, J., Petter, J., Petter, J., Newtson, J., Taneria, R., Taneria, R., Mard, Maczyk, R., Taneria, R., Mard, Maczyk, R., Mard, Maczyk, R., Mard, Maczyk, R., Mard, Maczyk, R., Mard, M., Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Williams, S., Wall, Martin,
                                            59070 TTGTAATGTACCAAGTCTTGCCAAAGAAGCAGAACAGCATTATGACACATTTTGTCAC 69011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO91418 245724 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-2G6, *** SEQUENCING IN PROGRESS ***.
AC091418
                                                                                                                                                                                                                                                                                                            410
                                                                                                                                                      294 ACGCCCCTCACGAGACACTGAACATGTGGTCACCGGCGAGACAGTGTGGCAATATTATCC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AGCTGGCTCCTAAT-AGGACAGTGCCAGTCCAATTCAAGCCCAGTCCTTTCTGTGTTTATT 469
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234 AAAAATGCAAGTGGATATTGAACAGTCTTCTTCTGATAATTCTAAATACAGTACAGTTC
                                                                                                                                                                                                                                                                                                        354 CIGIAATGTACCAAGTCTTGCCA---GAGCAGTGAACATTATGACACAACTTTTGTCAC
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 CCCATCTCCCAAATATTTGGAAACTGATGTCT 503
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AC091418/c
LOCUS
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.5409 ATTICAACCAAGGATGGATACTTAAGAAAATGTTGGCCAAATGAGTTATCTAGTGTTT 15350
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Rattus norvegicus clone CH230-24K10, *** SEQUENCING IN PROGRESS
***, 3 unordered pleces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                           176 CATAAGCAAGAGATTTAAGATTTTCCATTTAAGAA--GCCATTGTGAATTATACAACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15289 TTAAAAAGCAATCAATATTAAACAGTCTCTGCTCTGGTAATTCCAAATACTGTACAGTTC
                                                                                                                                     117 GATTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCCAAATAAGCTT-TCTGGTATTT
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HTG, HTGS. PHASEL; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission

Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON NOV 23, 2002 this sequence version replaced gi:2332270.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Arlas in the feature table below represents a craffold in the Arlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Milosavijevic, M. Mila, E., Montemayor, J., Moore, S., Milosavijevic, A., Minia, E., Montemayor, J., Moore, S., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Nair, L., Narker, S., Neal, D., Newton, N., Ngyren, N., Orris, S., Parker, N., Nayer, N., Orris, S., Parker, P., Popper, P., Polidexter, P., Polyovic, D., Primus, B., Pul. -L., Pazeternak, S., Pall, H., Perez, A., Perez, L., Pefannkoch, C., Pazeternak, S., Pall, M., Red, M., Reder, R., Reige, F., Riggs, F., Ruiz, S., Sanders, M., Quiroz, J., Rachlin, B., Reuter, M., Rose, M., Rose, K., Riggs, F., Rives, C., Rodkery, T., Rojas, A., Rose, M., Rose, M., Rose, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Svaterk, A., Trejos, Z., Usmani, K., Valas, R., Wars, M., Trejos, Z., Usmani, K., Wals, R., Wals, M., Willsams, B., Waldron, I., Walker, B., Wang, J., Walst, R., Wilson, R., Wals, M., Waright, D., Wright, R., Wu, J., Yakub, S., Yan, J., Yoon, L., Yoon, V., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Weinstock, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250169)
Rat Genome Sequencing Consortium.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hggc-help@bcm.tmc.edu
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

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Query Match
Best Local Similarity
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RESULT 13

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879407 682 bp DNA linear ROD 09-DEC-1995 mPPAR gamma 2=peroxisome proliferator-activated receptor gamma isoform 2 {promoter} [mice, Genomic, 682 nt].
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                                                                                                                                                                                                                                                                                                                                          Structural organization of mouse peroxisome proliferator-activated receptor gamma (mPPAR gamma) gene: alternative promoter use and different splicing yield two mPPAR gamma isoforms Proc. Natl. Acad. Sci. U.S.A. 92 (17), 7921-7925 (1995)
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Mus sp.

Mus sp.

Mus sp.

Mus sp.

Mammalia, Butheria, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.

1 (bases 1 to 682)

Zhu, Y., Qi, C., Korenberg, J.R., Chen, X.N., Noya, D., Rao, M.S. and

Reddy, J.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="mPPAR<gamma>2"
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isoform 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .682
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ROD 01-JUL-2003
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1. (pases 1 to 1160)
1. (pases 2 to 1160)
1. (props.M.x., Wittenburg,H., Li,R., Walsh,K.A., Leonard,M.R., Korstanje,R., Churchill,G.A., Carey,M.C. and Paigen,B. Liths Encompasses PPARgamma and SLC21Al Which Are Likely Genetic Determinants of Murine Cholesterol Gallstone Formation
                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 1160)
2 (bases 1 to 1160)
Lyons, M.A., Wittenburg, H., Walsh, K.A., Carey, M.C. and Paigen, B.
Direct Submission
Submitted (13-FBB-2003) The Jackson Laboratory, 600 Main Street,
Bar Harbor, ME 04609, USA
Location Qualifiers
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                                                                     Mus musculus strain DBA/2J peroxisome proliferator-activated receptor gamma transcript 2 (Pparg) gene, promoter region.
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Pred. No. 1.2e-40;
); Mismatches 86; Indels 16;
                                                       linear
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    ..1160
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/mol_type="genomic DNA"
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                                                      1160 bp
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transcript 2"
                                                                                                                                                            Mus musculus (house mouse)
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/gene="Pparg"
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Best Local Similarity 77.6%;
Matches 354; Conservative (
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 1159)
Lyons, M.A., Wittenburg, H., Li, R., Walsh, K.A., Leonard, M.R., Churchill, G.A., Carey, M.C. and Paigen, B.
Lithl3 Encompasses Lrpapl, Which is a Likely Genetic Determinant of Wurine Cholesterol Gallstone Formation
Unpublished
2 (bases I to 1159)
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                                                                                                                                                                                                                                                                                                    Lyone, M.A., Wittenburg, H., Walsh, K.A., Carey, M.C. and Paigen, B. Direct Submission
Submitted (25-PEB-203) The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="peroxisome proliferator-activated receptor gamma
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/chromosome="6"
                                                                                                        Mus musculus (house mouse)
                                                                      AY243584.1 GI:32395962
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1047 TTCCCACCTCTCCCAAATATTTGAAAACTGGTGTCT 1082

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Search completed: November 9, 2005, 02:15:43 Job time: 2644.94 secs

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1	503	100.0	2045	7	AAX19033	Aax19033 Human PP.
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7	52	10.3	177	7	AAX19064	Aax19064 Human PP
8	45.2	9.0	200000	12	ADO47191	Ado47191 DNA seq
o 0	44.2	8.8	3162	9	ABQ72637	Abg72637 Human MD
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c 11	41.8	8.3	93616	9	ADI03931	Adi03931 Human en
c 12	41.8	8.3	116297	12	ADQ97587	Adq97587 Human c
13	41.2	8.2	32392	9	ABL56203	Abl56203 AmEPV qe
c 14	40.8	8.1	2000	12	ADJ40655	Adj40655 Plant c
c 15	40.8	8.1	109661	12	ADQ97818	Adq97818 Human c
c 16	40.2	8.0	376	4	AAH93354	Aah93354 Human ch
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ABL70281 ABN80160	ABL33470	AAS46466	ABK31327	ABQ66998	AD143067	AD003207	ABZ10246	ABK28354	ABZ10162	ABZ10016	ADS89398	ADS89672	ABL21792	ABL55640	ABL56201	ADA02708	ADB72446	ADE95956	ADT05376	ADT05649	AAX84309	AAZ36928	ACN92690
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39.4	39.2	39	39	39	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.4	38.2	38.2	38.2	38.2	38.2	38	38	37.8	37.8	37.8
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ALIGNMENTS

Newly isolated nucleic acid comprising a control region of a human peroxisome proliferator activated receptor (PPAR) gamma gene - useful for identifying modulators that are useful in treating diseases associated with abnormal levels of human PPAR-gamma gene expression. Human; peroxisome proliferator activated receptor gamma; PPAR-gamma; regulatory sequence; promoter; obesity; anorexia; lipoma; cachexia; lipodystrophy; liposarcoma; human immunodeficiency virus; HIV; insulin resistance; non-insulin-dependent diabetes mellitus; polycystic ovary syndrome; gastrointestinal tract; Crohn's disease; inflammatory bowel disease; ulcerative colitis; bowel cancer; ss. oximal promoter, exon B and intron B. Auwerx J, Fajas L; Claim 10; Page 80; 102pp; English. 98WO-US015411. 97US-0053692P ntry) (LIGA-) LIGAND PHARM INC. (INSP) INST PASTEUR. Briggs MR, Saladin RS, WPI; 1999-142844/12. 25-JUL-1997; WO9905161-A1. 24-JUL-1998; Homo sapiens 04-FEB-1999.

The present invention describes an isolated, purified or enriched nucleic acid comprising a control region of a human peroxisome proliferator

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cortivated receptor gamma (PPDAR-gamma) gene. The nucleic acids are useful for secreening for agents capable of modulating the expression of a human PPDAR-gamma gene. These agents (modulators) (form pharmaceutical compositions that are useful for treating diseases associated with high/low levels of human PPDAR-gamma gene expression. The diseases include observing the cachexia, lipodystrophy, lipomas, lipomas. Ilpomas comes abnormalities associated with anti-human immunodeficiency virus (HIV) treatment, insulin resistance, non-insulin-dependent diabetes mellitus abnormalities associated with anti-human immunodeficiency virus (HIV) treatment, insulin resistance, non-insulin-dependent diabetes mellitus commander, insulin resistance, non-insulin-dependent diabetes mellitus tract, inflammatory bowel disease, Crohn's diseases of the gastrointeerinal (GI) tract, inflammatory bowel disease, Crohn's diseases ulcerative colitis and bowel cancer. The nucleic acids are useful for studying the role of PPAR-gamma enables genetic studies of PPAR-gamma mutations in humans, and elseases associated with altered adipose tissue function, like and elseases associated with altered adipose tissue function, like obesity and the production of transgenic animals, which are useful in screening for modulators of the human PPAR-gamma gene, which are useful in designing drugs for treating disorders or diseases associated with the level of PPAR-gamma gene expression. The present sequence with the level of PPAR-gamma - 2 proximal promoter, exon B and intron B
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100.0%; Pred. No. 2.5e-128;
ive 0; Mismatches 0;
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BP.

AAF23651 standard; cDNA; 1100

(first entry)

27-MAR-2001

AAF23651;

AAF23651 ID AAF7 XX AC AAF7 XX DT 27-N

RESULT 2

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Peroxisome proliferator-activated receptors (PPARs) are members of the nuclear hormone receptor subfamily of transcription factors. The present invention relates to antisense oligonucleotides (see AAF23652-F23731), targeted to a nucleic acid molecule encoding human PPARgamma, which specifically hybridises with and inhibits the expression of human PPARgamma. The present sequence is the coding sequence for the N-terminal sequence of human PPARgamma antisense oligonucleotides of the present invention can be used in the diagnosis and treatment of diseases associated with the expression of PPARgamma, e.g. to prevent or delay infection, inflammation or tumour formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antisense compounds capable of modulating expression of peroxisome proliferator-activated receptor gamma useful for diagnosis, prophylaxis and treatment of diseases associated with expression of the receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                Cytostatic, antiinflammatory; antisense oligonucleotide; PPARgamma; peroxisome proliferator-activated receptor gamma; transcription factor; nuclear hormone receptor; human; infection; inflammation; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACCAGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1100 BP; 334 A; 215 C; 195 G; 356 T; 0 U; 0 Other;
               Human PPARgamma N-terminal sequence coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Col 49-52; 40pp; English
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                                                                                                                                                                                                                                                                         18-JAN-2000; 2000US-00484345
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Best Local Similarity 96.8
Matches 488; Conservative
                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-070112/08.
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                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel nucleic acid from human chromosome 2 that shows altered expression in hyperplasia and/or tumours, especially of the thyroid. The invention describes a method for preparing nucleic acid that can be detected in thyroid cancers where these contain an absordescribes constructs comprising a fragment of the human DRIP gene and its splice variants, one of which contains all of exons 1-38 while the other lacks exons 27 and 28. Some tumours contain a fusion protein of DRIP, including a small segment from chromosome 3. The products of the invention have cytostatic and thyromimetic activity and are used for the inhibition of nucleic acid expression by antisense, ribozyme or RNA interference (RNA) methods. This sequence represents a fragment of human
                            479
 651
                                                      711
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                                                                                                                                                                                                                                                                                       hyperplasia; tumour; thyroid; cancer;
band 2p21-22; DRIP; cytostatic; thyromimetic;
TGTACCAAGTCTTGCCAAAGCAGTGAACATTATGACACAACTTTTTGTCACAGCTGGCTC
                         CTAATAGGACAGTGCCAGCCAATTCAAGCCCAGTCCTTTCTGTGTTTATTCCCATCTCTC
                                                      CTAATAGGACAGTGCCAGCCAATTCAAGCCCAGTCCTTTCTGTGTTTATTCCCATCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 85873 BP; 27329 A; 16422 C; 15988 G; 26134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid from human chromosome 2, useful for treatment and diagnosis of thyroid disease, especially cancer, also related polypeptides and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 85873;
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Pred. No. 1.3e-114;
                                                                                             CCAAATATTTGGAAACTGATGTCT 735
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                                                                                                                                                                                                                                                             Human chromosome 3p25 DNA fragment
                                                                              CCAAATATTTGGAAACTGATGTCT
                                                                                                                                                  RESULT 3
ADH10008/c
ID ADH10008 standard; DNA; 85873 BP.
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2002DE-01042705.
                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                      ds; human; chromosome 2;
break point; chromosomal
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                                                                                                                                                                                                                                                                                                                                              Synthetic
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TAGAGTAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACT

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8; Gaps

8; Indels

0; Mismatches

Matches 488; Conservative

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Local Similarity

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                                                                                                                                                                                                             54239 CAAGTGGATATTGAACAGTCTCTGCTCTGATAATTCTAAATACAGTACAGTTCACGCCCC
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                                               54359 CAACCAGGAATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA
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                                                                                                                      GCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATG
                                                                                                                                                                                          CAAGTGGATATTGAACAGTCTCTTCTCTGATAATTCTAAATACAGTACAGTTCACGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53999 CCAAATATTTGGAAACTGATGTCT 53976
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25-APR-2003; 2003US-0465241P.
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/standard_name= "Single nucleotide polymorphism"

Location/Qualifiers replace (145136, C)

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coronary artery disease; gene
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                                                                                                                                        JS2004043389-A1
                                 Homo sapiens
                                                                                                                                                                    04-MAR-2004
                                                              Key
variation
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                        The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatcoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA cand protein sequences of the invention are useful for disquassing and treating autoimmune diseases, such as rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, psornicious anaemia, asthma, vitiligo, glomerulonephitis, Grave's disease, anaemia, asthma, vitiligo, glomerulonephitis, Grave's disease, myocarditis, Ihe present sequence is not resent nucleic acid represents a human autoimmune disease-related control of the invention. NoTE: The present sequence is not control of the invention. NoTE: The present sequence is not control of the invention when the WIPO, whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                69124 ATGGATACAFATTTGAAFTCCAAATTTTTCTTCAAATAATGT-----GATTAGAGATT 69176
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                                                                                                                                                                                                                                                shown in the specification, but has been retrieved from the WIPO website
                                                                                                                                                                                                                                                                           Sequence 158417 BP; 47887 A; 30186 C; 31475 G; 48577 T; 0 U; 292 Other;
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Pred. No. 1.6e-114.
0; Mismatches 8
 Claim 16; SEQ ID NO 1675; 123pp; English
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ID ADLOB127/C
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AC ADLOB127;
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DE Human gene associated with low HDL-C
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KW Human; ds; SNP; single nucleotide po:
KW high density lipoprotein-C; HDL-C; vv
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Best Local Similarity
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The invention relates to determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises determining whether the subject has an allelic variant of a polymorphic region from any of 27 genes (alleles listed in Table 5 of the specification). Also included are determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the male subject has an allelic variant of a polymorphic region listed in Table 5 which is associated with abnormally con HDL-C levels in males, and determining whether a female subject has, or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the female subject has an allelic variant of a colymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in females. The allelic variant in determining whether a subject has, or is at risk of developing, an abnormally low HDL-C level complements. The allelic variant is at risk of developing, an abnormally low HDL-C level is at risk of developing, an abnormally low HDL-C level (GG, or their complements. The allelic variants are also COLSA2 (C GG, or their C GG, C C GG, or their complements. The allelic variants are also COLSA2 (C GG, Or their C GG, C C G GG, Or their C GMPL-C) in a complements. The methods are useful for diagnosing (a predisposition to) as undership as a variant and metable sassociated with abnormal liptid and metable metable of complements. The methods are useful in diagnosing (a predisposition to) are subject. The methods are useful in diagnosing (a predisposition to) are subject. The methods are useful in diagnosing (a predisposition to) are subject. The methods are useful in diagnosing (a predisposition to) are subject. The methods are useful in diagnosing (a predisposition to) are subject. The methods are useful in diagnosing (a predisposition to) are prognessicating the prognessicating and metable of low high density liptoprotein-C (
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                                                                                                                                                                                                                                                                                        Determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises detecting an allelic variant of a polymorphic region from any of a set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TAGAGTAAGTACTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACT
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Pred. No. 1.6e-114;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 46; 37pp; English.
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Best Local Similarity 96.8%;
Matches 488; Conservative C
(VITI-) VITIVITY INC
                                                                                                                                                                                            WPI; 2004-214170/20.
                                                                                                Mccarthy J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.
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Human; ds; SNP; single nucleotide polymorphism; high density lipoprotein-C; HDL-C; vascular disease; metabolic disease;

Human gene associated with low HDL-C PPARG.

the

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AAX19064 standard; DNA; 177
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                                                                                                                                                                                                                                  Matches 354;
                                                                                                                                                                                                                                                                                                                                                                  176
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                                                                                                                            145556 CAAGTGGATATTGAACAGTCTCTGCTCTGATAATTCTAAATACAGTACAGTTCACGCCCC 145497
                                                                                                                                                                                                                       145436 TGTACCCAAAGTCTTGCCCAAAGCAGTGAACATTATGACACACTTTTTGTCACACAGCTGGCTC 145377
                                                                                                                                                                                                                                                                          145376 CTAATAGGACAGTGCCAGCCAATTCAAGCCCAGTCCTTTCTGTGTTTTATTCCCATCTCT 145317
                145676 CAACCAGGAATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA 145617
                                                                            145557
                                                                                                                                                                                 145437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes established fat cell precursors with a DNA structure where the Stat5 gene is ligated in a state which allows its expression downstream of a promoter domain which can be induced by doxycycline. Also described: (1) screening compounds with an activity of controlling the induction of differentiation into fat cells comprising: (a) inducing the differentiation into fat cells in the fat cell precursors, (b) contacting a test compound with these cells after induction of their differentiation into fat cells; (c) measuring extent of the differentiation into fat cells; and (d) comparing
                                                                                                                                                         359
                                                                                                                                                                                                                                                             479
                                                                                                                                                                                                           419
CAACCAGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peroxisome proliferator activated protein-gamma-2 promoter SEQ:7.
                                                                                                                                                                       145496 TCACAAGACACTGAACATGTGGGTCACCGGCGAGACAGTGTGGCAATATTTTCCCTGTAA
                                                  GCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATG
                                                                          145616 GCAAGAGATTTAAGGTTTTCCATTTAAGAAGCAATTGTGAATTTTTACAACAATAAAAATG
                                                                                                                                                     TCACGAGACACTGAACATGT-GGTCACCGGCGAGACAGTGTGGCCAATATTATCCCTGTAA
                                                                                                                                                                                                          CTAATAGGACAGTGCCAGCCAATTCAAGCCCAGTCCTTTCTGTGTTTATTCCCATCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse, Stats, fat cell precursor, doxycycline, anorectic, obesity, peroxisome proliferator activated protein-gamma-2, promoter, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of established fat cell precursors for application in screening candidate compounds for controlling induction of differentiation into fat cells, useful in treating e.g. obesity.
                                                                                                                                                                                                                                                                                                                               480 CCAAATATTTGGAAACTGATGTCT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 56; 66pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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121
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ACC79611
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the extent of differentiation into fat cells with that observed in a control for evaluation of activity of the test compound, during which the order of steps (a) and (b) can be changed or carried out simultaneously before steps (c) and (d); (2) screened compounds inhibiting the differentiation of fat cell precursors into fat cells; and (3) screened compounds promoting the differentiation of fat cell precursors into fat cells. Staff as anorectic activity. The method is useful for the preparation of established fat cell precursors for application in screening candidate compounds for controlling induction of differentiation into fat cells, which are useful in treating e.g. obesity. The present sequence represents the mouse peroxisome proliferator activated protein-gamma-2 (PPAR-gamma) promoter, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       677 AAGAATGTGTATATGTTTGAGTACAAGAATATTTCTTCAGAT-GTGTGATTAG-----GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATAAGCAAGAGATTTAAGTTTTCCATTTAAGAAGCCA---TTGTGAATTAATACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 GATTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCCAAATAAGCTT-TCTGGTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     850 TTTAAAAAGCAATCAATATTGAACAATCTCTGCTCTGGTAATTCCAACTACTGTAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGCCCCTCACGAGACACTGAACATGT-GGTCACCGGCGAGACAGTGTGGCAATATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 ACAGCTGGCTCCTAAT-AGGACAGTGCCAACTCCAATTCAAGCCCAGTCCTTTCTGTGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 AACTATGGATACATATTTGAATTCCAAATTTTCTTCAGATAATGTGATTAGAGATTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 1184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1184 BP; 362 A; 227 C; 203 G; 392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 77.6%; Pred. No. 2.2e-49; 54; Conservative 0; Mismatches 86
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139429 TGAGAACAATGGAAAGCTTTTCTTCTAAGATAAGGAATAAGAAAAGAAATGCCCAGTCTTA 139488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139609 AACTTTATAAATTCCAAAAAATAAAATTCTGAAAAAAACAGCCACTGAAAACTAACAA 139668
                                                                                                                                                                                                                                                                                                                                                                                         New vector comprising one or more immunoglobulin regions selected from V, D, and J regions, a 5' flanking region, and a 3' flanking region, useful for reverting cell lines to a pro-B cell-like state or to a germline-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 TTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTTAAGTTTTTCCATTTAAGAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a method for the preparation of immunoglobulins. The method uses a vector for reverting cell lines to a pro-B cell-like state or to a germline-like state, by replacing one or more of the immunoglobulin regions V, D, and J of the rearranged immunoglobulin gene with the germ-line or unrearranged V, D or J regions. The vector can comprise a polymucleotide sequence encoding a recombination-promoting protein, selected from recombination activating gene 1 (RAG-1), RAG-2, terminal deoxymucleotidyltransferase (TdT). These proteins collectively constitute a V(D)J recombinase. The method is useful for the preparation of immunoglobulin heavy and/or light chains and their fragments. The present sequence encodes a human immunoglobulin heavy chain variable region, and is used as a template to construct vectors for use in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 TCAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGAATTCCAAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 200000 BP; 59904 A; 41194 C; 41535 G; 57367 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%; Score 45.2; DB 12; 48.1%; Pred. No. 0.19;
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                                                                                                                                                                                                                          (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 136-185; 382pp; English.
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                                                                                                             30-SEP-2003; 2003WO-AU001286.
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Matches 128; Conserv
WO2004029249-A1
                                                        08-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated, purified or enriched nucleic acid comprising a control region of a human peroxisome proliferator acid comprising a control region of a human peroxisome proliferator activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful for servening for agents capable of modulating the expression of a human PPAR-gamma gene. These agents (modulating the expression of a human CPPAR-gamma gene which acids as associated with high/low levels of human PPAR-gamma gene expression. The diseases include obesity, anorexia, cachexia, lipodystrophy, lipomas, lipodascomas, abnormalities associated with anti-human immunodeficiency virus (HIV) treatment, inflammatory bowel disease, non-insulin-dependent diabetes mellitus (NIDDM), polycystic ovary syndrome, disease, ulcerative colitis and bowel cancer. The nucleic acids are useful for studying the role of the PPAR-gamma enables genetic studies of PPAR-gamma enables genetic studies of PPAR-gamma enables genetic studies of PPAR-gamma mables genetic studies of PPAR-gamma mables genetic studies of PPAR-gamma in humans, and diseases associated with altered adipose tissue function, like and diseases associated with altered adipose tissue function, like for gene therapy and the production of transgenic animals, which are useful in designing drugs for treating disorders or diseases associated with the level of PPAR-gamma gene expression. The present sequence useful in designing drugs for treating disorders or diseases associated with the level of PPAR-gamma one expression. The present sequence tepresents the human PPAR-gamma one expression. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                      Newly isolated nucleic acid comprising a control region of a human peroxisome proliferator activated receptor (PPAR) gamma gene - useful for identifying modulators that are useful in treating diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin, B cell; germline; region V; region D; region J; recombination-promoting protein; recombination activating gene 1; RAG-1; RAG-2; 88; terminal deoxynucleotidyltransferase; TdT; V(D)J recombinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 GTCCTTTCTGTGTTTATTCCCATCTCTCCCAAATATTTGGAAACTGATGTCT 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCCTTTCTGTGTTTATTCCCATCTCTCCCCAAATATTTGGAAACTGATGTCT 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with abnormal levels of human PPAR-gamma gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 2; I
Pred. No. 0.00026;
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100.0%; Pred. No. v...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                  Fajas L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 87; 102pp; English.
                                                                                                                                                                                                                                                                                  Auwerx J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO47191 standard; DNA; 200000 BP
                                                                                  98WO-US015411
                                                                                                                                       97US-0053692P
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Best Local Similarity 100...
Best Local Si Conservative
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                                                                                                                                                                                            (LIGA-) LIGAND PHARM INC. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                               Saladin RS,
                                                                                                                                                                                                                                                                                                                                    WPI; 1999-142844/12.
                                                                                                                                       25-JUL-1997;
                                                                               24-JUL-1998;
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                          04-FEB-1999
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ADO47191;

RESULT

셤 8

Gaps

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Indels

Length 200000;

proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; hebumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthematic; antiatherosclerotic; antigout; neuroprotective; antirheumatic; antiatherosclerotic; antigout;

Homo sapiens.

WO200240715-A2

23-MAY-2002

06-SEP-2001; 2001WO-US027628

2000US-0230505P. 2000US-0230514P. 2000US-0230515P. 2000US-0230517P. 2000US-0230518P. 2000US-0229749P 2000US-0229750P 05-SEP-2000; 05-SEP-2000; 05-SEP-2000; 05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000;

2000US-0230595P. 2000US-0230988P. 2000US-0230597P 2000US-0230599P 2000US-023051

(INCY-) INCYTE GENOMICS INC

Flores V; Yap PE; Altus CM, Dufour GE, Chalup MS;
Yu JY, Wright RJ, Gietzen D, Liu TF,
Bradley DL, Rohatgi SD, Harris B;
EH, Peralta CH, David MH, Panzer SR, I
hen AJ, Chang SC, Au AP, Inman RR; Chen AJ, Gerstin EH, , Lincoln SE, Hill. Dahl CR, Moning. Roseberry AM, Gerstin en A, Marwaha R, (Jones AL, Hillman JL, Jackson S,

2002-527544/56 P-PSDB; ABP51420. Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.

Claim 1; Page 407-408; 618pp; English.

The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP5121-ABP518484) given in the sequence selected from 254 sequences (ABP5121-ABP51848) given in the section, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (II) (ABP07249-ABP72700) encoding (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology.

CN Nucleic acids (II) (ABP07249-ABP72700) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a bample, for detecting (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2722 CTATCAGAAATGAACTTTTTCCAGCTAATTCACTTCTATTAAGTAAACCAAGGAGCTTGA 2663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2602 GGCTTCAGAATTTTTATATGGTTATACAGGATCAGATTATGAGACTGTTGCAAACCT 2543
agonist or antagonist is useful for treating a disease or condition or suscotated with decreased or increased expression of functional MDDT. (I) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an arteriosclerosis, autoimmune/inflammatory disorder such as AIDS, Addison's disease, allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatorid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in sometic or type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2842 CTTCGAAATATAAAATATCTATAAATTTCTATGTACATAGTTTAAAAATTTTGAAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 GAACAGTCTCTCTCTGATAATTCTAAATACAGTACAGTTCACGCCCCTCACGAGACACT
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Pred. No. 0.092;
0; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.88;
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hes 145; Conservative
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ABL33191 standard; DNA; 6215 BP 26-MAR-2002 (first entry) RESULT 10 ABL33191/4

Human immune system associated gene SEQ ID NO: 1164.

Human; immune system disease; cytosine methylation; antiasthmatic; antiantiantamic; cytostatic; notropic; antianaemic; cytostatic; notropic; antiantamic; antiantamic; anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiantintianmatory; cancer; eye disease; arteriosclarosis; anamia; acute myeloid leukaemia; Alzhaimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;

Homo sapiens

WO200200928-A2.

03-JAN-2002.

02-JUL-2001; 2001WO-EP007537.

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Gan W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheijesy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGTATTTCATAAGCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATAC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAATAAAAATGCAAGTGTTTGAACAGTCTCTTCTCTGATAATTCTAAATACAGT 286
                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzyme protein; drug screening; disease diagnosis; human; gene therapy; chromosome 6; gene; ds; glucuronyltransferase.
                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful i
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.7%; Score 43.6; DB 6; Length 6215;
Best Local Similarity 58.5%; Pred. No. 0.17;
Matches 76; Conservative 0; Mismatches 54; Indels 0.
                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1164; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           '*tag= b
'product= "enzyme protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human enzyme protein encoding genomic DNA.
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2614. .96915
                                                                                                                        Berlin K;
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AD103931,C

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XX

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AD103931,3

XX

XX

XX

Expression (first entry)

XX

XX

Enzyme protein encoding ger

XX

XX

Chromosome 6; gene; ds; glucuron, occupation occ
                 30-JUN-2000; 2000DE-01032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4998 ATTATTCACG 4989
                                                                                                                      Piepenbrock C,
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                                                                              (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                   methylation.
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The invention relates to a novel isolated enzyme protein and encoding colymucleotides. The protein shows a high degree of similarity to a glucuronyltransferase cloned from a rabbit brain cDNA library. The glucuronyltransferase cloned from a rabbit brain cDNA library. The carelopment of human therapeutic targets, aid in the identification of therapeutic proteins, and serve as targets for the development of human the peptide may be used in drug screening assays, in the peptide may be used in drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies or to elicit another immune response, as a reagent in assays cantibodies or to elicit another immune response, as a reagent in biological for fluids, or as markers for tissues in which the corresponding protein is preferentially expressed. The human enzyme protein is also useful for diagnosing a disease, predisposition to a disease, or treating a disorder characterized by an absence of, inappropriate or unwanted expression of the protein. The antibodies are useful in pharmacogenomic analysis, for inhibiting protein function, or for tissue typing. The nucleic acid molecules are useful as probes, primers, chemical intermediates, or in min biological assays. The present sequence represents a human enzyme protein a biological assays. The present sequence represents a human enzyme protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human enzyme proteins, useful for treating or diagnosing disorders associated with abnormal expression of the protein, in drug screening
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50.8%; Pred. No. 1.3;
ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assays and pharmacogenomic analysis.
                      /number= 2
96603. .96751
                                                                                                                             /number= 3
96752. .96831
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/*tag= h
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26-MAR-2001; 2001US-00816095.
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Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                          WO200268657-A2
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vector; chromosome mapping; gene mapping;

(first entry)

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Novel recombinant entomopox virus vector useful for delivering polynucleotide encoding protein to vertebrate cell, comprises polynucleotide encoding protein operably linked with heterologous
                                                                    AmEPV; gene therapy; viral vecto
genetic deficiency disorder; ds.
                                                                                                        Amsacta moorei entomopoxvirus.
                                                                                                                                                                                                 10-AUG-2000; 2000US-0224479P.
14-SEP-2000; 2000US-00662254.
                                                                                                                                                                            10-AUG-2001; 2001WO-US025287
                                                                                                                                                                                                                                                           Moyer RW, Li Y, Bawden AL;
                                             AmEPV genome fragment#5.
                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                 WPI; 2002-227161/28.
                                                                                                                                                                                                                                                                                                                                              promoter sequence.
                                                                                                                           WO200212526-A2
                       01-JUL-2002
                                                                                                                                                    14-FEB-2002
ABL56203;
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                                                                  AMEPV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 TGATACCAACGTTTAAACTATGGATACATATTTGAATTTCCAAATTTTTCTTCAGATAATG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GCTTTCTGGTATTTCATAAGCAAGAGATTTAAGGTTTTCCATTTAAGAAGCCATTGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 116297 BP; 33950 A; 22909 C; 23278 G; 36160 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.8; DB 12; Length 116297;
                                                                                                                                                                            Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Indels
                                                                                                                                                    Human cancer associated sequence HD10-009, SEQ ID 564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Scc...
50.8%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 564; 199pp; English.
                                                                     587/c
ADQ97587 standard; DNA; 116297 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16709 AAGGAAAAAGTAACAA 16693
                     8710 AAGGAAAAAGTAACAA 8694
222 TATACAACAATAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 TATACAACAATAAAAA 238
                                                                                                                                                                                                                                                                      22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                                                                                                                              27-DEC-2002; 2002US-00330773
                                                                                                                                                                                                                                                                                                                    (SAGR-) SAGRES DISCOVERY INC
                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                           Morris DW, Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-543781/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                        WO2004060304-A2.
                                                                                                                                                                                                   Homo sapiens.
                                                                                                                             07-OCT-2004
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                                                                                                    ADQ97587
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The invention relates to a recombinant entomopox virus (EPV) vector, comprising a polynucleotide encoding a protein operably linked with a comprising a polynucleotide encoding a protein also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein cinvention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in vitro or in vivo. The vector is useful for the delivery and expression of particle, or by transfection, transduction, or injection either in vitro or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for engineering of vertebrate cells. Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation provide for stable integration and expression of heterologous DNA in host provide for stable integration and expression of heterologous DNA in host provide for stable integration and expression of the invention of sense or antisense nucleic acids. Vectors of the invention provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polynucleotide inserts which can be delivered in an infected or transformed cell and expressed in a stable fraction. The current sequence represents a correction amsacta moorei fragment of the genome of the genus B entomopoxvirus from amsacta moorei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4783 TTÄTACATÄTÄÄÄCTTAATTÄTTÄTATTÄÄTTÄTTÄTTATAATÄÄTÄTÄTGÄÄÄTTÄTC 4842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4903 TATCTTGTCAAAATTTATTATAAAAAATTATATAGTGTATTTTATGGAATAGATTATA 4962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 TGAATTCCAAATTTTTTTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 ACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32392 BP; 13748 A; 2577 C; 2550 G; 13517 T; 0 U; 0 Other;
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Pred. No. 1.
Disclosure, Page 226-242; 326pp; English.
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ABL56203 standard; DNA; 32392 BP.

RESULT 13 ABL56203 ID ABL5 XX

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The invention relates to plant nucleotide sequences that direct seed.,

leaf- and/or stem., panicle., root- or pollen-specific or -preferential

or constitutive transcription of an operatively linked nucleic acid

segment. The invention also relates to a method for augmenting a plant

genome and a method of identifying a gene, where its expression is

altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,

cancia, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

sorghum, rice or wheat. The polymucleotides and the polypeptides they

concide are useful for manipulating crop plants to alter or improve

phenotypic characteristics, to produce large quantities of oil or

proteins, to incur resistance to insecticides, viruses or fungi, and to

cincur stress tolerance (e.g. salt, cold or drought) to ensure the plants

carly flowering or altered metabolic pathways. This sequence represents a
                                                                                                                                                                                                                                           Plant; gene; se; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolarance; salt tolarance; cold tolarance; drought tolarance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                             4963 AAAATATAAATAAATAATTTAAAAATATATGTAAAAAGGATTTAAA 5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glazebrook
194 GTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T, Briggs SP, Cooper B, Glaz
Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; SEQ ID NO 1655; 230pp; English.
                                                                                                                ADJ40655 standard; cDNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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Katagiri F,
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATAGIRI F.
KREPS J.
PROVART N.
                                                                                                                                                                              (first
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                                                                                                                                                                                                              Plant cDNA #1655.
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ZHU T.
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04-APR-2002;
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                                                                                                                                                                                                                                                                                                                                antifungal
                                                                                                                                                                                                                                                                                                                                                               Eukaryota
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(RICK/)
(ZHUT/)
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(KREP/)
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(COOP/)
(GLAZ/)
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1937 ATTTCGTATGATAAACATAGAAAATAAATATAAGATGATGAGATGTGTTCTTTCAACTAAAT 1878
                                                                                                                                                                                                                                                                                 1877 GACACGATTTTGTATGCTTCATATATTGCATATTTTATAATCATCGAGAAACTATAAG 1818
                                                                                                                                                                                                                                                                                                                                                     1817 CAÁTTGÁGÁTGATTTGCTTTÁTGÁTATÍTTAGÁTCAÁATATTGCÍTGATCGTCTAÁAGGÁ 1758
                                                                                                                                                                                                                                                                                                                                                                                         243
plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                         184 AGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAA
                                                                                                                                                                            AGTAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATG
                                                                                                                                                                                                                                                GATACATATTTGAATTCCAAATTTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAA
                                                                                                                                                                                                                                                                                                                    CCAGGGATAGACACCGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCA
                                                                                                                                           Gaps
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                                                                                                      Length 2000;
                                                                   Sequence 2000 BP; 540 A; 381 C; 366 G; 713 T; 0 U; 0 Other;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer associated sequence HD11-002, SEQ ID 795
                                                                                                      Score 40.8; DB 12;
Pred. No. 0.69;
0; Mismatches 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2003; 2003WO-US041389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-DEC-2002; 2002US-00330773.
                                                                                                                         48.0%;
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                                                                                                                         Best Local Similarity 48.0
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-543781/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1697 ATGG 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 GTGG 247
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                                                                                                                                                                                                                                                                                                                     124
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                                                                                                        Query Match
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ADQ97818/c
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196 TTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAAATGCAAGTGGATATTGAA 255
                                                          76 AATTCCAAATTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAGAC 135
                                                                                                                     136 ACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGT 195
                                0; Gaps
Query Match 8.1%; Score 40.8; DB 12; Length 109661; Best Local Similarity 50.5%; Pred. No. 2.5; Matches 99; Conservative 0; Mismatches 97; Indels 0; C
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Sequence 15491, A
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-94-016-15492

1 Sequence 15492. Application US/09949016

2 Sequence 15492. Application US/09949016

3 Sequence 15492. Application US/09949016

3 GENERAL INFORMATION:

4 APPLICANT: VENTER, J. Craig et al.

7 TILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

7 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

7 CURRENT PELLING DATE: 2000-04-14

7 PRIOR FILING DATE: 2000-04-17

7 PRIOR PELLING DATE: 2000-10-03

7 PRIOR FILING DATE: 2000-10-03

7 PRIOR FILING DATE: 2000-10-03

7 PRIOR FILING DATE: 2000-09-08

8 NUMBER OF SEQ ID NOS: 207012

8 SOCTHARE: PRESECE for Windows Version 4.0

8 SEQ ID NO 15492
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Pred. No. 1.1e-123;
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Best Local Similarity 96.8
Matches 488; Conservative
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Sequence 15491, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15491

LENGTH: 86877
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592 TGTACCAAGTCTTGCCAAAGCAGTGAACATTATGACAACTTTTTTGTCACAGCTGGCTC 651
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Pred. No. 1.1e-123;
0; Mismatches 8; Indels 8;
                                                                                                                                                                CCAAATATTTGGAAACTGATGTCT 503
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Best Local Similarity 96.8
Matches 488; Conservative
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Sequence 3, Application US/09816095
Sequence 3, Application US/09816095
Patent No. 6664084
GENERAL INFORMATION:
ADDILIANT: GRAN, Weiniu
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1147
CURRENT PILLING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOPTWARE: FastSEQ for Windows Version 4.0
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                                                          61 CTAATAGGACAGTCCAGCCAATTCAAGCCCAGTCCTTTCTGTGTTTATTCCCATCTCTC 120
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Sequence 22, Application US/09806708B

Patent No. 6784342

GENERAL INFORMATION:
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REPRENCE: 4810-58741

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/147,133

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.0
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50.8%; Pred. No. 0.15;
tive 0; Mismatches 97; Indels 0;
                                                                                                             480 CCAAATATTTGGAAACTGATGTCT 503
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LOCATION: (1)...(99916)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
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LENGTH: 99916
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       Sequence 133111, Application US/09949016

Patent No. 6812339
GENERAL INPORMATION.
GENERAL INPORMATION.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastesQ for Windows Version 4.0
SEQ ID NO 133111
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Batent No. 6812339

GENERAL INFORMATION:
Patent No. 6812339

GENERAL INFORMATION:
PLICANT: URBYING.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PaseLSEQ for Windows Version 4.0
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Matches 143; Conservative
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Matches 143; Conservative
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US-09-949-016-133111
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NAME/KEY: promoter to LOCATION: (1)..(1141) COTHER INFORMATION: CONSENSUS SEQUENCE Of A.t., L.a., and B.n. FAEI promoters US-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 TTAGAGATTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11111 1111 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 WEWHWYTVDYTMMRAWNNNNNNWRBCKTTSWMWMDHMYTHCTYGNNTWGSAYBMAAMS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 RDTTCTYVDVWADSWVWWYANWMRCRDVTYTRNNTYCKSYAHSYWYWYRNAMWYRRYSAR 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 ATTICATAAGCAAGAGITTTAAGTTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TAAAAATGCAAGTGGATATTGAACAGTCTCTTCTCTGATAATTCTAAATACAGTACAGT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 TCACGCCCCTCACGAGACACTGAACATGTGGTCACCGGCGAGACAGTGTGGCCAATATTAT 351
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Sequence 23, Application US/09806708B

Patent No. 6744342

GENERAL INFORMATION:
PAPLICATION OF British Columbia

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

FILE REFERENCE: 4810-58741

CURRENT PELING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Version 3.0

SEQ ID NO 23

TENCH 10 23
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; OTHER INFORMATION: consensus sequence of A.t. and L.a. FAE1 promoters
US-09-806-708B-23
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                                                                                                                                                                                                                 DB 4; Length 1141;
                                                                                                                                                                                                    Query Match 8.0%; Score 40.4; DB 4; Length 1 Best Local Similarity 9.0%; Pred. No. 0.062; Matches 37; Conservative 175; Mismatches 197; Indels
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ORGANISM: Artificial sequence
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Best Local S
Matches 55
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JUNE OF THE PAPELICATION NUMBER: 60/231, Application US/09949016

Bequence 12572, Application US/09949016

Betent No. 681233

GENERAL INFORMATION:

JUNEATION:

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US-09-949-016-16366
US-09-949-016-16366
Sequence 16365 Application US/09949016
Sequence 16365 Application US/09949016
Sequence 16365 Application US/09949016
Sequence 16365 Application US/09949016
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FIRE REPREBRUES CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                                                              158 ATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGTTTTTCCATTTAAGAAGCCATTGT 217
                                                                                                                                                                                                                                                                                                  79 TCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAGACACC 138
505 YWGNAMWYAAYSAGNTSSMARWTTANNTAAGGYMRAAWAGTMWAAMANNNNTRTRYYAWW 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 GAAAGAAAACTITIGCCCAAATAAGCTITICTIGGTATITICATAAGCAAGAGATITAAGTTTT 198
                                                                                                                                      GAATTATACAACAATAAAAATGCAAGTGGATATTGAACAGTCTCTTCTCTGATAATTCT
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Pred. No. 0.89;
0; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                              278 AAATACAGTACAGTTC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 WITTWWAAAISWWKWY 310
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Best Local Similarity 47.9%;
Matches 112; Conservative (
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; ORGANISM: Human
US-09-949-016-12572
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Sequence 13001, Application US/09949016
; Sequence 13001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTICATION WINDHERS: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-00-08
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESE 
                                                                                                                                  24180 TAATATTATATATATATATATATATATATATATATAAACATTGGTGGCATCTCACA 24121
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                                                                                                                                                                                                                                                  126 AGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAG
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                                                                                                                                                                                                                                                                                                           186 AGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAAGT
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                             4; Gaps
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Best Local Similarity 49.8%; Pred. No. 2;
Matches 126; Conservative 0; Mismatches 123; Indels
                          Mismatches 123; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13001
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                          Matches 126, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(13626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 IGATACCAACGITITAAACIAIGGAIACAIAITITGAAITICCAAATITITICITICAGAIAAIG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38.4; DB 4; Length 108310;
Pred. No. 1.6;
0; Mismatches 131; Indels 0;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PABEISEQ for Windows Version 4.0
SEQ ID NO 16366
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Pred. No. 2;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12756
LENGTH: 136264
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; Sequence 12756, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(136264)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.6%;
Best Local Similarity 47.2%;
Matches 117; Conservative
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Best Local Similarity
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Gape

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APPLICATION VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREUSEQ for Windows Version 4.0

SEQ ID NO 15830

LENGTH: 192506
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                                             212203 AATAATGATCATTATGTTATAAAATTAATGCATCTAAAAAAGTTTTTAAAAAACAGTTC 212144
                                                                                                                                                                                                                                 191028 GGAAGAGACCATTTAACTCTCCAACAATAGTGACATCAAGAAATGACACCAATTGTTG 190969
    ATACCAACGTTTAAACTATGGATACATATTTGAATTCCAAATTTTTCTTCAGATAATGTG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 ATTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAGACA 136
                                                                                                                                                                                      TITCIGGIAITICATAAGCAAGAGAITITAAGITITICCATITIAAGAAGCCATIGIGAATIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 GGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 37; DB 52.2%; Pred. No. 5.1; ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-15830/c
. Sequence 15830, Application US/09949016
. Patent No. 6812339
. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               TACAACAATAAAAAT 239
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Best Local Similarity
Matches 82; Conserv
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ORGANISM: Human
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                                                                                 US-01-218-796A-1010

Sequence 1010, Application US/09248796A

Patent No. 674137

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUMBER: US/09/248,796A

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 1010

LENGTH: 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 TITCATAAGCAAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 ATGGAGTATTAATAATAATGATTTTAAATTACAAAAACTAATGAAATTAAAAATTAAT 803
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APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTONI, MASAHIRA
APPLICANT: SATAKI, YOSHIYUKI
FILE REFERENCE: 081356/0129
FILE REFERENCE: 081356/0129
CURRENT FILING DATE: 2001-02-23
PRIOR PILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 AAAAATGCAAGTGGATATTGAACAGTCTCTTCTCTGATAATTCTAAATA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 37.6; DB 4; Length 640681;
49.5%; Pred. No. 5.6;
tive 0; Mismatches 99; Indels 0;
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Best Local Similarity 47.8%; Pred. No. 0.34;
Matches 110; Conservative 0; Mismatches 120; Indels
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Patent No. 6632935
24120 AGTAACTCCACAT 24108
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Matches 97; Conserva
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CORGANISM: Buchnera
US-09-790-988-1
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US-09-790-988-1/c
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8, 2005, 18:06:53; Search time 650.857 Seconds (without alignments) 6391.142 Million cell updates/sec
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Sequence 46, P
Sequence 31, P
Sequence 189,
Sequence 1164,
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(9GDZ 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
(9GDZ 6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
(9GDZ 6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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(9GDZ 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
(9GDZ 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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(9GDZ 6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-235-192A-46
US-10-672-74A-31
US-10-363-829-189
US-10-311-455-1164
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Listing first 45 summaries
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8.8 3162
8.7 6215
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US-10-181-176-10

Sequence 10, Application US/10181176

Sequence 10, Application US/10181176

Publication No. US2050186567A1

GENERAL INFORMATION:

APPLICANT: Robert McKay

APPLICANT: Brenda F. Baker

TITLE OF INVENTION: ANTISENSE MODULATION OF PEROXISOME PROLIFERATOR-ACTIVATED RECEPTO

TITLE OF INVENTION: GAMA EXPRESSION

FILE REFERENCE: RTSP-0328

CURRENT APPLICATION NUMBER: US/10/181,176

CURRENT APPLICATION NUMBER: US/10/181,176

CURRENT FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: US/484,345

FRIOR PLING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 90

SEQ ID NOS: 90
                                                                                             Sequence 5619, Ap
Sequence 5661, Ap
Sequence 36653, A
Sequence 18984, A
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28, Appl
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197296,
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                      US-10-634-905-3

US-10-706-635-27

US-10-20-238-1655

US-10-741-601-5661

US-10-41-601-5661

US-10-41-601-5661

US-10-43-126-240

US-10-674-124A-1055

US-10-674-124A-1055

US-10-674-124A-1055

US-10-674-124A-1055

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US-10-925-065A-861470

US-09-925-065A-37192

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US-10-473-126-386

US-10-67-632-299

US-10-67-632-299

US-10-027-632-197296

US-10-027-632-197296

US-10-052-483-214

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US-10-052-483-214
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US-09-925-065A-676914
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; NAME/KEY: CDS
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US-10-181-176-10
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90.5%; Score 455.2;

Query Match

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TYPE: DNA ORGANISM: Human
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US-10-363-829-189/c
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LENGTH: 200000
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US-10-672-764A-31
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US-102A-46/C
US-10-235-192A-46/C
Sequence 46, Application US/10235192A
Sequence 46, Application US/10235192A
Sequence 46, Application No. US20040043389A1
GENERAL INFORMATION:
APPLICANT: MCCARCHY, Jeaneth Compositions for Identifying
TITLE OF INVENTION: Methods and Compositions for Identifying
TITLE OF INVENTION: And Disorders Associated Therewith
FILE REFERENCE: MMI-011
CURRENT APPLICATION NUMBER: US/10/235,192A
CURRENT FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
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                                                                   239 TAGAGTAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACT 298
                                                                                               ATGGATACATATTTGAATTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATT 120
                                                                                                                          299 ATGGATACATATTTGAATTCCAAATTTTTCTTCAAATAATGT-----GATTAGAGATT 351
                                                                                                                                                      CAACCAGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA 180
                                                                                                                                                                      CAACCAGBAATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAA 411
                                                                                                                                                                                                              GCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATG 240
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 Pred. No. 1.6e-108;
0; Mismatches 8;
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al Similarity 96.8%;
488; Conservative
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Matches 488; Conservative
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ORGANISM: Homo sapiens
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Publication No. US20040156832A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Jolly, Chris
TITLE OF INVENTION: Immunoglobulin Compositions and Methods
FILE REFERENCE: 13311.1001U
CURRENT APPLICATION NUMBER: US/10/672,764A
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ 10 NOS: 68
SOFTWARE: FASESEQ for Windows Version 4.0
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48.1%; Pred. No. 2.6;
tive 0; Mismatches 138;
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Best Local Similarity 48.13
Matches 128; Conservative
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CURRENT PILING DATE: 2003-03-05
FRIOR PILING DATE: 2001-09-05
FRIOR PILING DATE: 2001-09-05
FRIOR PILING DATE: 2001-09-05
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                                                                                                           APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Wright, Rachel J.; Gitzen, Darryl;
APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Marwaha, Marie H.; Panser, Scott R.;
APPLICANT: Chang, Vincent Z.; Daffo, Abel;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Inman, Rebekah R.
APPLICANT: Inman, Rebekah R.
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Pred. No. 0.79;
0; Mismatches 168; Indels 0;
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US-10-363-829-189
Sequence 189, Application US/10363829
Publication No. US20040142331A1
GENERAL INFORMATION:
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Best Local Similarity 46.3%;
Matches 145; Conservative (
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ORGANISM: Homo sapiens
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LENGTH: 3162
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Sequence 1164, Application US/10311455

Sequence 1164, Application US/10311455

Sequence 1164, Application US/3030143606A1

Sexure US20030143606A1

Sequence 1164, Application US/3030143606A1

SEXURAL INFORMATION: US20030143606A1

APPLICANT: DISPERBRENCK, Christian

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APPLICANT: DEBERBROCK, Christian

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APPLICANT: GAN, Weiniu
TITLE OF INVENTION:
TITLE OF INVENTION: THEREOF
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253 GAACAGICTCTTCTCTGATAATICTAAATACAGTACAGTTCACGCCCCTCACGAGACACT 312
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8.7%; Score 43.6; DB 16;
Best Local Similarity 58.5%; Pred. No. 1.5;
Matches 76; Conservative 0; Mismatches 54;
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Patent No. US20020137164A1
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                        313 GAACATGTGGTCA 325
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                                                                 TYPE: DNA
ORGANISM: Human
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US-10-634-905-3/c
Sequence 3, Application US/10634905
Sequence 3, Application US/10634905
Sequence 3, Application OS US20040067225A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UNMBER: US/10/634,905
CURRENT APPLICATION NUMBER: US/10/634,905
CURRENT APPLICATION NUMBER: 203-08-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FABLESC for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 99916
                                                                                                                                                                                                                                                                                                                                                                                              8770 AGTACATTTCTTGCAAAAAAAAAATTTTTTTTTTTAATGTAATAACATTAACAAA 8711
                                                                                                                                                                                                                                       8890 idraacraacacarrangeacacargiacceraaaacrraaagrarararaaaa 8831
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                                                                                                                                                                                                                                                                                 162 GCTTTCTGGTATTTCATAAGCAAGAGTTTTAAGTTTTCCATTTAAGAAGCCATTGTGAAT 221
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                                                                                                          Query Match 8.3%; Score 41.8; DB 9; Length 99916; Best Local Similarity 50.8%; Pred. No. 15; Matches 100; Conservative 0; Mismatches 97; Indels 0;
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8.3%; Score 41.8; D
Best Local Similarity 50.8%; Pred. No. 15;
Matches 100; Conservative 0; Mismatches
NAME/KEY: misc_feature

LOCATION: (1)...(99916)

COTHER INFORMATION: n = A,T,C or G

US-09-816-095-3
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LOCATION: (1)...(99916)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 8

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APPLICANT: Moyer, Richard W.

APPLICANT: Li, Yi
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APPLICANT: Li, Yi
APPLICANTON: Waterials and Methods for Delivery and Expression of Heterologous
TITLE OF INVENTION: Waterials and Methods for Delivery and Expression of Heterologous
TITLE OF INVENTION: VMMER: US/10/706,635
CURRENT APPLICATION NUMBER: US/10/706,635
CURRENT FILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-29
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
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8.2%; Score 41.2; DB 22;
Best Local Similarity 48.7%; Pred. No. 13;
Matches 112; Conservative 0; Mismatches 118;
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US-10-706-635-27
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Sequence 27, Application US/10706635
Publication No. US20050014263A1
GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
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APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
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Provart, Nicholas
Ricke, Darrell
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; NAME/KEY: misc_feature
; LOCATION: (1)...(101782)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5661
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18-10-477-963-36633/C

## Sequence 36633/C

## Sequence 3633/C

## Sequence 363/C

## Sequence 3
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                                                                                                                                                                                          Sequence 5661, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOOLSO
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 5661
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8.1%; Score 40.8; DB 20; Length 1
Best Local Similarity 50.5%; Pred. No. 27;
Matches 99; Conservative 0; Mismatches 97; Indels
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// LOCATION: (1)...(59914)
// CHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-741-601-5619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35452 CATGAAAAAATTTTTAAGTAAATTAGAATACTGCAAATGCATAATAAACAGCTTTAAAT 35511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35392 ACTTCCAAGTATGTTTATAAATATATATGTCTAAAACCATTAAGGTTGAGAAAATATACTG 35451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1937 ATTTCGTATGATAAACATAGAAAATAAATATAAGATGAAGATGTGTTCTTTCAACTAAAT 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1877 GACACGATTTTGTATGCTTCATATAATTGCATATTTTATAATCATCGAGAAACTATAAA 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1817 CAÁTTGÁGÁTGATTTGCTTTÁTGÁTAÍTTTAGÁTCAÁATAÍTGCÍTGÁTCGÍCTAÁAGGÁ 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GATACATATTTGAATTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 CCAGGGATAGACACCGAAAGAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 AGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AATTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAGAC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAAGTGGATATTGAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AGTAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATG 63
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Sequence 5619, Application US/10741601

Sequence 5619, Application US/10741601

Sequence 5619, Application US/10741601

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

PILE REPERENCE: CL001500

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOUTWARE: PASSECTION OF SECTION                                                                                                                                                                                                                                                                                                                                                                                                ö
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8.1%; Score 40.8; DB 20; Length 59914;
Best Local Similarity 50.5%; Pred. No. 22;
Matches 99; Conservative 0; Mismatches 97; Indels 0;
                                                                                                                                                                                                                                                                                               Length 2000;
                                                                                                                                                                                                                                                                                          8.1%; Score 40.8; DB 18; Length
48.0%; Pred. No. 5;
tive 0; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35572 CACAGICICCAGIGIT 35587
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                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 48.03
Matches 117; Conservative
                                                                                               ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GTGG 247
SEQ ID NO 1655
LENGTH: 2000
                                                                                                                                                                                                                                                                                               Query Match
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Distance between 3'-terminus of neighbour sequence of sequence listing upward to telomere on chrosomal short arm 5'-terminus of this base sequence : 158826
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                                                                                                                                                                                                                                                                                           135 CACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAG
                                                                                                                                                                                                                                                                                                                                                                           15 TAGGAATATAACATTICAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Distance between a terminus base of telomere on chromosomal short arm and 5'-terminus of this base sequence : 111170513
                                                                                                   ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 21; Length 8056;
Pred. No. 15;
0; Mismatches 115; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: chrl.fa.O7frz.118358138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1055, Application US/10674124A Publication No. US20040197797A1 GENERAL INFORMATION:
                     LENGTH: 8056
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                  8.0%;
                                                                                                                                                                  Query Match
Best Local Similarity 48.73
Matches 109; Conservative
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OTHER INFORMATION:
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INFORMATION:
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  SEQ ID NO 240
LENGTH: 8056
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                                                                                    FEATURE:
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US-10-473-126-240/c

US-10-473-126-240/c

US-10-473-126-240/c

US-10-473-126-240/c

Sequence 240, Application US/10473126

Publication No. US20040234973A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell

TITLE OF INVENTION: proliferative disorders

TITLE OF INVENTION: proliferative disorders

TITLE OF INVENTION: DATE: 2003-09-26

CURRENT APPLICATION NUMBER: US/10/473,126

NUMBER OF SEQ ID NOS: 1258
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18984, Application US/10424599
Publication Wo. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihna
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION WUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/203-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 18984
LENGTH: 797
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                                                                                  114 AGAGATTCAACCAGGGATAGACACCGAAAGAAACTTTGCCCAAATAAGCTTTCTGGTAT 173
                                                                                                                         217 AAAAATTGCACCAATGCTAGAATCAGATGGAGAGCTGTTCAATAAAGATATGCTGATAT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 TTTAAACTATGGATACATATTTGAATTCCAAATTTTTCTTCAGATAATGTGATTAGAGAT 112
                                                                                                                                                                174 TTCATAAGCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGAATTTTTTTAAATAAATTTTAGAATCTTTTATACATTTAATTTTATTAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 TAGAGATTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITCATAAGCAAGATITAAGITITCCATITAAGAAGCCATIGIGAATTATACAACAAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 ATTAATAGTTAAAAAAACTTGGTATTTAATTGAATAGTGTGTTTTAGATGTTTATACAGT 472
                                                                                                                                                                                                  157 ATACACATCAAGGGTTTCAAATTTTCTACATTATACTCCATTCATGTATTTCCAATCACA 98
                                             Gaps
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    DB 20; Length 1886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTGAAAATTAAAAATTTGGTATTTAATTGAATGATGTATTTAGAT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 797;
Score 40.4; DB 20; Length Pred. No. 6.2; 0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.0%; Score 40.2; DB 19; Length Best Local Similarity 48.5%; Pred. No. 4.9; Matches 111; Conservative 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_117146C.1
                                                                                                                                                                                                                                                  234 AAAATGCAAGTGGATATTGAACAGTCTCTTCTC 267
                                                                                                                                                                                                                                                                                         AGAACAGAATGCAGCATATGTTCAGTTTGCTATC 64
ch
1 Similarity 53.9%;
83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-424-599-18984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-18984
Query Match
Best Local S
Matches 83
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Indels

7.9%; Score 39.8; DB 20; 50.8%; Pred. No. 4.3; tive 0; Mismatches 92;

Query Match
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3 170		83
·	=	TTATTCCAG
111 ATTAGAGATTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCCAAATAAGCTTTCTG	_ = =	\TTATATATATATATATATATATATATATATATATATTTTCAACACAATTTCTTATTCCP
AAAACTTTG	_ _	ATATTTCAA
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²³¹ ATAAAAA 237

^{|| || || |} 28 ATGAATA 22

Search completed: November 8, 2005, 23:53:31 Job time: 652.857 secs

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CH261-810 dab28d09. BP623936

CC273164 BG438771 BP623936 BU811789

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taj19b03. GROAAA36D

Drosophi]

CL110860 CV464338 CR812616 AL096962 CC273164 BG438771 BP623936

Drosophil BONGG6OTF Drosophil 894041C12 SCJFHR103

ALIGNMENTS

Drosophil odh08h10.

EUGI1789 CCL934409 CCL934409 CCBG0244 AL06257 AL067453 AL09163 BEX609163 BEX60917301 BEX38026 CCA104351 BEX38026 CCA104351 BEX38026 BEX38026 BEX38026 BEX38026

CNS00ZB7 BH970382 CNS010MP

CL934409 CB180244 BZ601497 CNS00EJ4

BZ469037 CNS0026Z BE238266 CA104351 BI738064

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- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl' and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR28W18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Modoteryqota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
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/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
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BH957102 odj02b02.
AL059515 Tetraodon
BH46086 BCGSK22TF
AL059666 Drosophil
CC764640 CH244 47
CL33525 RPC144 25
AL166396 Drosophil
BH742342 gV74b05.9
BZ46575 BOHYL59TF
BH661305 BOHYL59TF
AG61305 BOHYL59TF
AG61305 Drosophil
CB88081 taa87b01.
AL06363 Drosophil
CL88428 AB652544 Drosophil
CL88428 AB652512.
BH711021 BOMFC41TF
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OR_BBa000
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(c) 1993 - 2005 Compugen Ltd.
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Score 51.6; DB 9; Length 1101; Pred. No. 0.011;

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8 셤 ઠે 용

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BH957102 747 bp DNA linear GSS 01-OCT-2002 odj02b02.bl B.oleracea002 Brassica oleracea genomic genomic survey
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                                                                                                                                                                                127 GGGATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGA 186
                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  187 GATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAAATGCAAGTG 246
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Delehaunty K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
Seq primer: -21UPpOT forward
class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                   247 GATATTGAACAGTCTCTTCTCTGATAATTCTAAATACAGTA 287
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High quality sequence stop: 551.
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- Web : www.genoscope.cns.fr |
- Web : www.genoscope.cns.fr |
- Web : www.genoscope.cns.fr |
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoscar in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRi digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be located of the library found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                          130 ATAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGT 189
                                                                                                                                                                                                                                                      TTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAAATGCAAGTGGAT 249
                                                                                                                                                                                                                                                                                                      870 TTAHTTWTKATWTWYCCGRNTCWSTAGAGACMRASACMSASAGAMYMTHMMAKAYT 929
                                                                                                                                                                                                                                                                                                                                                        250 ATTGAACAGTCTCTTCTCTGATAATTCTAAATACAGTACAGTTCACGCCCCTCACGAGAC 309
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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  73; Mismatches 118; Indels
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COMMENT

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                                                                                                       /clone lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. Day was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Obborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 raatarataaraaaraararataargerittirarataaraaaaarargararaca 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 TATTIGAATICCAAATITITCTICAGATAATGIGATIAGAGATIAGAGATICAACCAGGG 129
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/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                       CNSO4LKI 1106 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 118P23 of library G from Tetraodon nigroviridis, genomic survey
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777 AAAAAAAWIWITUTITITITCCITTAAAAAACTITACAACAWCAAAWITITIYWIAAA 836
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                          Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="G"
/note="Genoscope sequence ID : C0BG118CH12LP1~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 ATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGAATT
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11.4%; Pred. No. 0.41;
Ive 24; Mismatches 140; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Tetraodon nigroviridis"
"mol_type="genomic DNA"
(db_kref="taxon:99883"
/clone="118P23"
                                                                                                                                                                                                                                                                                                          AL296235.1 GI:8034815
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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Conservative
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                                                                                                            231 TTAAATTTACAA 242
                                                                          190 TTAAGTTTTCCA 201
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Matches 116; Conserv
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AUTHORS
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KEYWORDS
SOURCE
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837 ACAAAWAATTYTTCACACAATTTWACAAAAAAAATTWWTAYCATCATAAAAAACAACCT 896
                                                                                                897 YYTAAAAACTIYTIAAAAHYWTITIAWIWACCITITITIAACTIYYTAAAAAAACYYTIT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH460886 766 bp DNA linear GSS 13-DEC-2
BOGSK22TF BOGS Brassica oleracea genomic clone BOGSK22, genomic
                                                                                                                                                     200 CATTTAAGAAGCCATTGTGAATTATACAACAATAAAAATGCAAGTGGATATTGAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 ATTICAGIAGCATGCTGATACCAACGITIAAACTATGGATACATATTIGAATTCCAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 766)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 GAAGCCATTGTGAATTATACAACAATAAAAATGCAAGTGGATATTGAACAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.7;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                             1017 TTTBTTTTTTTTAWTTTATTWAAAWAAACAAACACCC 1056
                                                                                                                                                                                                                                                              260 CTCTTCTCTGATAATTCTAAATACAGTACAGTTCACGCCC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .766
/organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="TO1000DH3"
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/clone="BOGSK22"
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Contact: Chris Town
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Class: sheared ends.
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Best Local Similarity 49.4
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              survey sequence.
BH460886
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LOCUS DEFINITION

RESULT 6 CNS00CS1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS JOURNAL

TITLE

COMMENT

REFERENCE

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Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.B., de Jong, P.J. and Lewin, H.A.

Bovine BAC end sequences from CHORI-240 library
Unpublished (2003)
Octher GSSS: CH240 47L12.TV
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewindwinc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bowine BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AC202-34480-11828
CH240 47L12.TJ CHORI-240 Bos taurus genomic clone CH240_47L12, CH240_67L12, CH240_47L12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                452 TITAAAATITICAAAAAAGCACAAAATACAAATATGTAAAATITIGAAACATCTTAAATT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 GAGAAGAATATATAAATATGCTTTTATATGATTGAGCTCTTATAGGTTCTATTCCTAT 273
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 TATAACATTICAGTAGCATGCTGATACCAACGTTTAAACTATGGATACATATTTGAATTC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /coll type="Blood"
/coln=lib="CHORI-240"
/note="Vector: pTARBACI.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 AAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGTTTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 43.2; DB 9; Length 495; 50.0%; Pred. No. 1.5; tive 0; Mismatches 108; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 ATTTAAGAAGCCATTGTGAATTATACAACAATAAAA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db xref="taxon:9913"
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Plate: 47 row: L column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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                                                                                                                  CC764640
CC764640.1 GI:32311143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 495)
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Matches 108, Conservative
                                                                                                                                                                                                      Bos taurus (cow)
Bos taurus
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                              LOCUS
DEFINITION
                                                                                                                                                                                                   SOURCE
ORGANISM
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   CC764640/c
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JOURNAL
COMMENT
                                                                                                                  ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage : Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage : PRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr |
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buiffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digetion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                             BACOSOPHILA melanogaster genome survey sequence TET3 end of BAC # BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit AL059666
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
/clone="BACR26H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                         AL059666.1 GI:4947129
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
ATACCAACGITIAAACIAIGGAIACAIAITIGAAIICCAAAITITICIICAGAIAAIGIG 103
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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/mol type="genomic DNA"
/db Xref="taxon:7227"
/clone="BACN15M24"
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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8.6%; Score 43.2; DB 9;
Best Local Similarity 41.5%; Pred. No. 1.8;
Matches 102; Conservative 22; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: schook@uluc.edu
Clones are derived from the porcine BAC library RPCI-44
(http://www.bacpac.chori.org/porcine242.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@chori.org).
Clones may be purchased from BACPAC Resources
(http://BACPACorders.chori.org). This work was undertaken as part
of the International Swine Genome Sequenciing Consortium by
University of Illinois at Urbana Champaign, USA with funds provided
by grant No. AG2002-34480-11928 from USDA-CSREES and
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
                                                                                                                  CL335225 618 bp DNA linear GSS 19-AUG-2004 RPCI44 253A15.r RPCI-44 Sus scrofa genomic clone RPCI44 253A15, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 618)
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/etrain="four pigs (breed: 37.5% Yorks Landrace and 25%
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/clone lib="RPCI-44"
/note="Vector: pTARBAC2; Site_1: EcoR1; Site_2: EcoR1;
porcine male BAC library produced by Pieter de Jong"
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48.3%; Pred. No. 1.6;
tive 0; Mismatches
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clone="RPCI44_253A15"
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Sus scrofa
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Class: BAC ends.
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Matches 117,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clohe lib="BoBudsol" x reads, pBluescript for .b and .g /note="Vector: M13 for .x reads, pBluescript for .b and .g reads, Site 1: BcoRv, Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prepusing Brassica oleracea Tol000DH3 buds provided by Thomas provided by Pablo Rabinowicz (GSHL) and shotgun library prepared in McCombie Lab."
en، مراوعة 623 bp DNA linear GSS 25-FEB-2002
gu74b05.g1 BoBuds01 Brassica oleracea genomic clone gu74b05 5',
genomic survey sequence.
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                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, eudicotyledons, core eudicots, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, 10 solds, eurosida I; Brassicales, Brassicaceae, Brassica.

(bases 1 to 623)

Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Kuit,K., Miller,B., Muller,S., Nascimento,L., Kirchoff,K., Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and McCombie,W.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGACACCGAAAGAAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTIATAAATAGCAATITICCATAAAATTATTACGAAATTGCCTAATATTAGCTACCT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 TTGCAATCCATAAAAAACTATAAAATACATTAAATTATCAGATTAATTCATTGTTTATT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAAATGCAAGTGGATA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                               Whole Genome Shotgun Reads from Brassica oleracia (2002b) Unpublished (2002) Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory Po Box 100, Cold Spring Harbor Laboratory Tel: 516 367 8884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone="gu74b05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 623.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mccombie@cshl.org
Plate: gu74 row: b column: 05
Seq primer: -21UnivRev
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Matches 126; Conservative
                                                                                                                              Brassica oleracea
                                                                                                                                                Brassica oleracea
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RESULT 11

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669 bp DNA linear GSS 13-DEC-2002 BONMO35TF BO 1.6.2 KB tot Brassica oleracea genomic clone BONMO35, genomic survey sequence.
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Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids; eurosida II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="BONMQJS" /clone lib="BONMQJS" /clone lib="BO 1.6 2 KB tot" /note="Vector: pHoS1, Site 1: BstX1; 1.6-2 kb sheared total DNA inserted into pHŌS1 using BstX1 linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TAAGTACCTTAGGAATATAACATTTCAGTAGCATGCTGATACCAACGTTTAAACTATGGA
                                                                                                                                                                                                                                                                                                                1 (bases 1 to 669)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Wholb genome shotgun sequencing of Brassica oleracea Other GSSs: BONMQ35TR
Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301-838-3523
Fax: 301-888-0208
Email: cdrown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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Class: sheared ends.
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Brassica oleracea
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Seq primer: TF
Class: sheared ends
      Fax: 301 838 0208
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RPCI-11-326P5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-326P5,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 Tricraactaaaccaraaacaaarriraaacirrrararacararrircaaarcaaaraa 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAAAATATAATACAGAGCCCAATTTGAAATACCAACTCAAATTATGGTTTTTATATTTA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 766)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.'.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 CTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGTTTTCCATTTAAG
                                                                                                                                                                                                                                                                                                                                                 /clone="BOHYL59"
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genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                        Tel: 301-838-3523
Fax: 301-838-3528
Email: odtown@tigr.org
Email: odtown@tigr.org
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.4%; Score 42.4; DB 8; Length 818; Best Local Similarity 47.7%; Pred. No. 2.7; Matches 124; Conservative 0; Mismatches 136; Indels
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Cother GSSs: RPCI-11-326PS.TV
Cother GSSs: RPCI-11-326PS.TV
Cother CSSs: RPCI-11-326PS.TV
Cother Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
                                                                                              Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                       organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                               db_xref="taxon:3712"
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                                                            Contact: Chris Town
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Spermatophyta; Magnollophyta; Enbryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 874)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Unpublished (2002)
Other GSSS ZUARQ48TH
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ZUAAC48TV ZM_3.0_4.0_KB Zea mays genomic clone ZMMBPa0005G23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
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Email: hbeetigg.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pleter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: SP6

Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 AAGCAAGAGATTTAAGTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 AÁTTÁGCAGATCAÁGGCTATAAÁTATTTTTÁGGGCTCTTGÁTTTÁATÁTTÁTTGÁTÁAÁTTG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
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RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 CTATGGATACATATTTGAATTTCCAAATTTTTCTTCAGATAATGTGATTAGAGATTAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526 CTATTGCTGTATAAACAAATTATTTATTTTGTTACTATAATATCACTAGAAATATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 TTCAACCAGGGATAGACACCGAAAGAAAACTTTGCCCCAAATAAGCTTTCTGGTATTTCAT
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Pred. No. 3;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 TGCAAGTGGATATTGAACAGTCTCTTCTCTGATAA 273
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                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG019400.1 GI:33891565
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Best Local Similarity 49.8%;
Matches 107; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
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Genoscope.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter do Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is anamed RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://wagac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                  ö
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/clone_llb="ZM 3.0 4.0 KB"
/note="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA llbzary"
                                                                                                                                                                                                                                                                                                                                                                                                                   84 ATTTTTCTTCAGATAATGTGATTAGAGATTAGAGATTCAACCAGGGATAGACACGGAAAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AAAACTTTGCCCAAATAAGCTTTCTGGTATTTCATAAGCAAGAGATTTAAGTTTTCCATT 203
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 3.1;
0; Mismatches 98;
                                                                        /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence. AL063632
                                                                                                                              db_xref="taxon:4577"
                                                   organism="Zea mays"
location/Qualifiers
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50.8%;
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                                                                                                                                                                                                                                                                                                                                               CAAGAGATTTTAAGTTTTTCCATTTAAGAAGCCATTGTGAATTATACAACAATAAAAAATGC 241
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                                                                                            Length 1101;
                                                                                                                            Matches 108; Conservative 37; Mismatches 146; Indels
                                                                                        Query Match 8.4%; Score 42.2; DB 9;
Best Local Similarity 37.1%; Pred. No. 3.3;
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/note="end : TET3"
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		υ	25	50.6
OM nucleic - nucle:	OM nucleic - nucleic search, using sw model			50.6
		υ		50.4
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	(without alignments)			50.2
	7308.644 Million cell updates/sec		30	50.2
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Perfect score: 125	111	υ		50.2
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		O	35	20
Scoring table: ID	SNIIIX NUC	U	36	50
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Searched: 43	4390206 segs, 2959870667 residues			49.8
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2:	geneseqn1990s:*	AAX1	AAX19032	
3:	genesequ2000s:*	ΩI	AAX19	AAX19032 st
4	geneseqn2001as:*	X		
50	geneseqn2001bs:*	AC	AAX19032;	032;
9		×		
7:		DT	13-MA	13-MAY-1999
80	geneseqn2003as:*	X		
.60	ס	DE	Human	Human PPAR-
10:		X		
11:		ΚM	Human	Human; pero
12:		ΚM	regul	regulatory
13:		KW	lipod	lipodystrop
		KW	insul	insulin res

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Query Match	* Query Match Length DB	DB	ΙD	Description
1	125	100.0	503	~	AAX19032	Aax19032 Human PPA
0	118.6	94.9	12548	13	ADS36487	Ads36487 Human aut
m	118.6	94.9	158417	13	ADS36461	Ads36461 Human aut
4	81.4	65.1	201	~	AAX19063	Aax19063 Human PPA
c S	57.8	46.2	1416	æ	ABZ20967	Abz20967 Animal te
ω υ	56.6	45.3	420	13	ACN51217	Acn51217 Cotton an
7	54.4	43.5	1315	~	AAZ41312	Aaz41312 Human nor
60	54.2	43.4	200	Ŋ	ABV61578	Abv61578 Human pro
0	54.2	43.4	629	13	ACN54594	Acn54594 Cotton an
10	53	42.4	1131	12	ADQ23807	Adq23807 Human sof
c 11	52.2	41.8	168	9	ABN69641	Abn69641 Streptoco
c 12	52	41.6	3163	10	ADC87060	Adc87060 Human GPC
13	52	41.6	28198	2	ADG37080	Adg37080 Mouse pla
c 14	51.8	41.4	344	4	AA182007	Aai82007 Human pol
c 15	51.8	41.4	437	13	ACN58918	Acn58918 Cotton gy
c 16	51.4	41.1	110000	12	ADQ97050 0	Adq97050 Human can
c 17	51.2	41.0	349	4	AAI84504 _	Aai84504 Human pol
c 18	, 51	40.8	588	13	ACN54596	Acn54596 Cotton an
19	51	40.8	900	9	ABQ52497	Abq52497 Oligonucl
c 20	51	40.8	009	9	ABQ52496	Abq52496 Oligonucl

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cc activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful CC for screening for agents capable of modulating the expression of a human PPAR-gamma gene (modulators) form pharmaceutical compositions that are useful for treating diseases associated with high/low levels of human PPAR-gamma gene expression. The diseases include high/low levels of human PPAR-gamma gene expression. The diseases include cobesity, anorexia, cachexia, lipodystrophy, lipomas, lipoasrcomas, abnormalities associated with anti-human immunodeficiency virus (HIV) treatment, insulin resistance, non-insulin-dependent diabetes mellitus composition overy syndrome, diseases of the gastrointestinal (GI) tract, inflammatory bowel disease, Crohn's disease, ulcerative colitis and bowel cancer. The nucleic acids are useful for studying the role of the PPAR-gamma enables genetic studies of PPAR-gamma male genetic studies of PPAR-gamma male genetic studies of PPAR-gamma enables genetic studies of PPAR-gamma matations in humans, and diseases associated with altered adipose tissue function, like and diseases associated with altered adipose tissue function, like obesity and lipodystrophic syndromes. The nucleic acids consein and assays. The control regions of the nucleic acids consolise acreening assays. The control regions of the nucleic acids consolise acreening descreening disorders or diseases associated with the level of PPAR-gamma-lip proximal promoter, exon Al and intron Al expresents human PPAR-gamma-lip proximal promoter, exon Al and intron Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCCTGCCCCTGCCCCTGCCCCCACCCCCACCCCCACCCCCACCCCCAGCCGGCGCCCGC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human autoimmune disease-related genomic DNA sequence - SEQ ID 1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 125; DB 2; Length 503; 100.0%; Pred. No. 7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 503 BP; 60 A; 184 C; 211 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism detection; SNP detection;
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ID ADS36487 standard; DNA; 12548 BP
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25-APR-2003; 2003US-0465241P.
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The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention. The DNA and protein sequences of the invention are useful for diagnosing and treating autoimmune disease, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, pernicious anneamia, asthma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sjogran's disease, or primary systemic vasculitis. The present nucleic acid represents a human autoimmune disease-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                            shown in the specification, but has been retrieved from the WIPO website
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
                                                 New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.9%; Score 118.6; DB 13; Length 12548; 96.8%; Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12548 BP; 3528 A; 2769 C; 2492 G; 3757 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                       the invention. NOTE:
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                                                                                                                                               Claim 16; SEQ ID NO 1701; 123pp; English
                                                                                                         diseases, e.g. rheumatoid arthritis.
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25-APR-2003; 2003US-0465241P.
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Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence of
                   WPI; 2004-728480/71
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25-JUL-1997;
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                                                                                                                                                                                 genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention act useful for disposing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, poriasis, tyroniditis, cellac disease, pernicious ansemia, asthma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sjogren's disease, or primary systemic vasculitis. The present nucleic acid respresents a human autoimmune disease related genomic DNA sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the NIPO website.
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158417 BP; 47887 A; 30186 C; 31475 G; 48577 T; 0 U; 292 Other;
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                                                                             New isolated nucleic acid molecule comprises at least 8 contiguous
                                                                                                                                                                          The invention comprises amino acid and coding sequences containing
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 158417;
                                                                                          nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118.6;
                                                                                                                                               Claim 16; SEQ ID NO 1675; 123pp; English.
                         Alexander HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PPAR-gamma-1 proximal promoter.
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Matches 121; Conservative
                         Cargill M, Begovich AB,
(APPL-) APPLERA CORP.
                                                    WPI; 2004-728480/71.
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The present into present in solutions and isolated, pointing of comprising a control region of a human peroxisome proliferator activated receptor gamma (PPRR-gamma) gene. The nucleic acids are useful for scenning for agents (modulators) form pharmaceutical compositions that are useful for treating diseases associated with high/low levels of human PPAR-gamma gene expression. The diseases include obesity, anorexia, cachexia, lipodystrophy, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, lipomas, li
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                                                                                                                                                                                                                                                                                                                                                                                         Newly isolated nucleic acid comprising a control region of a human peroxisome proliferator activated receptor (PRAR) gamma gene - useful identifying modulators that are useful in treating diseases associated with abnormal levels of human PPAR-gamma gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 CCGACCCGGTT---CCGCCGCGGGCAGGCGGGCCCCAGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGACCCGGATCCGCCGCGCGCGGGCAGGCGGGCCCAGC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents the human PPAR-gamma-1 proximal promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.1%; Score 81.4; DB 2; 96.0%; Pred. No. 0.00032; ive 0; Mismatches 1
                                                                                                                                                                                                                   Auwerx J, Fajas L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 87; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers replace (581,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Animal test kit marker DNA 127-sp6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ20967 standard; DNA; 1416 BP
97US-0053692P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                  (LIGA-) LIGAND PHARM INC. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                   Saladin RS,
                                                                                                                                                                                                                                                                                                           WPI; 1999-142844/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Local s.
95; '
                                                                                                                                                                                                                        Briggs MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus.
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ID ABZ209
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24-JUN-2004
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                                                                                                                                                                                                                                                                                                                 The present invention relates to a new test kit comprising marker DNA, for cattle or derived meat products, which has any of the sequences shown in AB220937-AB220970, all of which contain at least one variable position (single nucleotide polymorphism, SNP), and these SNPs are tabulated. The kit is used in animal production or breeding, and to track cattle-derived foods, e.g. for consumer protection. The specified sequences contain sufficient SNPs, present at various frequencies in the cattle population, to provide, in combination, a genetic fingerprint for individual animals. The variable positions can be queried by high-throughpur methods, making possible typing of the entire cattle population in the form of a digital DNA signature. The present sequence is a bovine marker DNA for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                            bovine marker DNA, useful e.g. in animal breeding and comprises specified polymorphic sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium; variety Nocotton; bloary LIBS828; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ceceraceceraceceracececacececacececacececacececacececace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cotton androecium tissue EST Clone ID: LIB3828-011-01-N6-H6, SEQ:5998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.2%; Score 57.8; DB 8; Length 1416; 66.4%; Pred. No. 0.7; ive 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1416 BP; 270 A; 253 C; 540 G; 348 T; 0 U; 5 Other;
                                                                                                                                                                                                                                              Test kit containing bovine marker DNA, for tracking foods, comprises specifie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACN51217 standard; cDNA; 420 BP
/*tag= a
replace(697,A)
/*tag= b
                                                                                                                                                                                                                                                                                         Claim 1; Page 18; 25pp; German.
                                                                                                                14-MAR-2002; 2002DE-02006477
                                                                                                                                            2002DE-01012560.
2002DE-02006477.
                                                                                                                                                                                        (GAGB-) GAG BIOSCIENCE GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             test kit of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                   WPI; 2003-048092/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                          DE20206477-U1
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Local Sim-
83; C
                                                                                                                                            14-MAR-2002;
14-MAR-2002;
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                                                                                     10-OCT-2002
                variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
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셤 ò 셤 ò 셤

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US2004123340-A1.

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The invention relates to 17880 cotton expressed sequence tags (ESTS);
ACM45220-ACM5099). The ESTS were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DP50B, mature seeds from
C variety Coker 312 Boswell 36 Field, and androcedium tissue, gynoecium
C tissue, developing fibres, carpel walls and septa from variety
C buccton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
C comprising a nucleic acid of the invention. The cotton ESTS are useful
C invention, and to transformed plants having a nucleic acid construct
C comprising a nucleic acid of the invention. The cotton ESTS are useful
C comprising a nucleic acid of the invention. The cotton ESTS are useful
C comprising a nucleic acid of the invention. The cotton ESTS are useful
C comprising a nucleic acid of the invention. The cotton ESTS are useful
C cused for isolating a variety of agronomically significant genes
C members of a particular gene family. The nucleic acid molecules may be
C used for isolating a variety of agronomically significant genes
C also useful for identifying genes important in intriating and maintaining
C seed germination or that may be used to mitigate stresses encountered
C during seed germination. The ESTS additionally enable the acquisition of
C during seed germination. The ESTS additionally enable the acquisition of
C componentially significant genes in these tissues are further useful for
C schemes, genetic and molecular mapping, and in cloning of agronomically
C significant genes. The nucleic acid molecular markers useful for a
C detecting the expression level or pattern of a protein or mRNA and for
C detecting the expression level or pattern of a protein or wall for detecting the value priminal and sequence represents a specifically claimed EST isolated from a
C cotton variety Nuccetton31B enderseles and in cloimed EST isolated from a parent is the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 coccreccoraccocyreccocaccoccaccoccaccoccaccoccagocagocago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to 17880 cotton expressed sequence tags (ESTs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCCCGCCCCCGCGCCCGGCCCGGCCCGACCCGGTTCCGCCGCGGGC 111
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45.3%; Score 56.6; DB 13; Length 420;
Best Local Similarity 69.4%; Pred. No. 1.5;
Matches 77; Conservative 0; Mismatches 34; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                     Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5998; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                          Fincher KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ41312 standard; cDNA; 1315 BP
                                                                                    14-DEC-2000; 2000US-0255619P.
12-DEC-2001; 2001US-00021323
                                                                                                                                                                                                                                                                                                                                                                                          Feng PCC,
                                                                                                                                                                    DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to map genes.
                                                                                                                                                                                                                                                                                                                                                                                     Deikman J,
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                                                                                                                                                                                                                                                         (FINC/) (ZIEG/)
                                                                                                                                                                    (DEIK/)
(FENG/)
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed in normal ovary tissue. Artificial diremosomes and cosmid clones containing the sequences can be used as gene transfer vehicles. The sequences can be used to produce DNA fragments containing full-length genes. Host cells transformed with the sequences can be used to produce polypeptides or polypeptide fragments, which can be used to screen phage displays for polypeptides that bind to them, or as tools for identifying agents active against ovarian cancer, or to prepare medicaments for treating ovarian cancer. The cDNA sequences can be used to obtain genomic sense, their promoters enhancers, allencers, exon structures, intron structures and their splice variants. AAA4122-Z4124 represent cDNA sequences derived from normal human ovarian tissue and which encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCCTGCCCCTGCCCCTGCCCCCACCCCCACCCCCCACCCCCAGCCGGGCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel nucleic acid sequences that are highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                      Dahl
                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequences potentially useful in diagnosis or therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCCCGCCCCCCGCCGCCCGGCTCGGCCCCGACCCCGGTTCCGCCGCGGCA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54.4; DB 2; Length 1315;
Pred. No. 2.3;
0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                      Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1315 BP; 355 A; 320 C; 228 G; 412 T; 0 U; 0 Other;
                                                                                   Human; ovary; screening; ovarian cancer; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein fragments represented in AAY59724-Y59837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate expression marker cDNA 61569.
                                                Human normal ovarian tissue derived cDNA 91
                                                                                                                                                                                                                                                                                                   (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                      Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 201; 274pp; German.
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                                                                                                                                                                                                                                                               98DE-01016395
              (first entry)
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Best Local Similarity 67.9
Marches 76; Conservative
                                                                                                                                                                                                                                                                                                                                      Rosenthal A, Specht T,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-552352/47
                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian cancer.
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                                                                                                                      Homo sapiens
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                18-JAN-2000
                                                                                                                                                                                           07-0CT-1999,
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The invention relates to an isolated nucleic acid molecule (I) comprising a mucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cotton; plant; BST; expressed sequence tag; transgenic plant; androecium; variety Nucotton338; library LIB3828; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 céceccécececécececacececécececentaria a consecente de consecente de consecente de consecente de consecente de consecente de consecente de consecente de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consecuta de consec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 11665-11666; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monahan JE
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2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                                    2000US-0183319P.
2000US-0189862P.
                                                                                          20-FEB-2001; 2001WO-US005171
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ID ACN54594 standard; cDNA; 629
                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0255281P
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Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gossypium hirsutum
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                                                                                                                                                                                                                                                                          25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000;
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                                                                                                                                                                                                                                            16-MAR-2000;
23-AUG-2001
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Ginsburg WM,
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                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                      10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                   Aziz N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN69641/c
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACN45220-ACN63099). The ESTB were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DPSDB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
Nucotton33B. The invention also relates to substantially purified
proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
comparising a nucleic acid of the invention. The cotton ESTB are useful as
molecular tags to isolate genetic regions, to isolate genes are
members of a particular gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes are
associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination. The ESTS additionally enable the acquisition of
promorers and cis-regulatory elements which will be useful to express
also permits the acquisition of molecules are further useful for
also permits the acquisition of molecules are further useful for
detecting the expression level or pattern of a protein or makes
chemes, genetic and molecular mapping, and in cloning of agronomically
significant genes. The nucleic acid molecules are further useful for
detecting the expression level or pattern of a protein or makes
cotton variety Nucleorian appoing, and in cloning of agronomically
sequence data for this patent did not form part of the printed
sequence data for this patent did not form part of the printed
sequence data for this patent did not form part of the brinted
specification, but was obtained in electronic format directly from the US
patent office at sequate or patents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCCTGCCCTGCCCCTGCCCCCACCCCCACCCCCACCCCCAGCCCCCAGCCGGCGCCCCGC 60
                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54.2; DB 13; Length 629;
Pred. No. 3;
0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 629 BP; 29 A; 38 C; 562 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                 Ziegler TE;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 9375; 34pp; English.
                                                                                                                                                                                                 Fincher KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ23807 standard; DNA; 1131 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.4%;
                                         14-DEC-2000; 2000US-0255619P
12-DEC-2001, 2001US-00021323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Conservative
                                                                                                                                                                                               Deikman J, Feng PCC,
                                                                                   DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                           WPI; 2004-479808/45.
                                                                                                                                                                                                                                                                                                                                                          tags to map genes.
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                                                                                                       (FENG/)
(FINC/)
(ZIEG/)
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                                                                                     (DEIK/)
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(first entry)

26-AUG-2004

ADQ23807

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and sarcoma-upregulated bNA of the invention. The current sequence is not a human soft tissue sarcoma-upregulated bNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GCCCGCCCCCCCCGCCCCGGCCCCGACCCGGTTCCGCCGCGGCGCAGCGGGGCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 12; Length 1131;
Pred. No. 3.9;
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Human soft tissue sarcoma-upregulated DNA - SEQ ID 6627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 6627; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROT-) PROTEIN DESIGN LABS INC.
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55.7%;
                                                                                                                                                                                                                                                                                                                                           26-NOV-2003; 2003WO-US038193
                                                                                                                                                                                                                                                                                                                                                                                                     26-NOV-2002; 2002US-0429739P
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Best Local Similarity 55.7°
Matches 68; Conservative
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JP2003189850-A.
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                                                         EP1270724-A2
                                    Homo sapiens
                                                                                  02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG37080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                              Exceptococcus (3BS (Streptococcus agalactiae) or group A streng stock of Streptococcus agalactiae) or group A streng stock of Streptococcus agalactiae) or group A strengtococcus (3BS (Streptococcus agalactiae) or group A strengtococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. biological sample. (1) is used to detect Streptococcus in a biological sample. (1) is used to detecnime whether a compound binds to used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity
                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCCTGCCCCTGCCCCTGCCCCCACCCCCACCCCCACCCCCAGCCGGGGGGCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a protein (ABP25413-ABP30895) from group B
group A streptococcus, Streptococcus pyogenes; antibacterial; gene, antiinflammatory, infection, vaccine, meningitis; gene therapy; ds.
                                                                                                                                                                                                                      Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCCCGCCCCCGCCCGGCCCGGCTCGGCCCCGACCCGGTTCCGCCGG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches 34; Indels
                                                                                                                                                                                                                      Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 168 BP; 4 A; 4 C; 147 G; 7 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.2; DI
Pred. No. 8.5;
                                                                                                                                                                                                                     Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 3875; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  060/c
ADC87060 standard; DNA; 3163 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GPCR gene SEQ ID NO:1513.
                                                                                                                                27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.8%;
67.3%;
                                                                                                         29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 67.3 es 72; Conservative
                                                                                                                                                                                                                      Masignani V,
                                    Streptococcus agalactiae
                                                                                                                                                                                             INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins
                                                                                                                                                                                                                                                         WPI; 2002-352536/38.
P-PSDB; ABP29010.
                                                                                                                                                                                  (CHIR-) CHIRON SPA
                                                         WO200234771-A2
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                                                                                                                                                                                                                    Telford J,
Tettelin H;
                                                                                  02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC87060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                              (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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셤
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triphosphate-binding protein coupled receptor (GPCR). A polymucleotide of the invention may have a use in gene therapy. The polymucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polymucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
ds; gene; human; GPCR;
guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to a novel polynucleotide encoding a guanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3163 BP; 340 A; 345 C; 1360 G; 610 T; 0 U; 508 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 3163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animal cell; beta-catenin; plakoglobin; cadherin adhesion; signal transduction; cross-reactivity; desmosome cadherin; Wnt signal transduction; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels
                                                                                                                                                                                                                                                                                                                                                                                           (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse plakoglobin polynucleotide seq id 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1513; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВЪ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suwa M, Asai K, Akiyama Y,
                                                                                                                                                                                                                                                                   18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.8
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-315783/31.
P-PSDB; ADC87061.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, call proliferation or call differentiation or which may induce production of other cytokines in other call populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem call growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium; variety Nucotton338; library LIB3829; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cotton gynoecium tissue EST Clone ID: LIB3829-013-Q6-N6-G12, SEQ:13699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 cccrrecccrrecccrreccccacccccacccccacccccaccccaagccacccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 344;
                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2067; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 344 BP; 33 A; 26 C; 225 G; 40 T; 0 U; 20 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
41.4%; Score 51.8; DF
Best Local Similarity 61.2%; Pred. No. 8.1;
Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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26-FEB-2001; 2001WO-US004927
                                           28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                   Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004 (first entry)
                                                                                                                                                                                                                    WPI; 2001-514838/56.
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                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                           P-PSDB; AAO02076
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                                                                                                                                                                                                                                                                                                                                                                           The invention describes an animal cell which has defective or lack of expression of beta-catenin and/or plakoglobin. The cell is useful for research purposes. The beta-catenin defective cell, plakoglobin defective cell or the beta-catenin and plakoglobin defective animal cells are useful for studying the function and regulation mechanism beta-catenin and/or plakoglobin, for analysing the diseases, disorders or conditions resulting from the variation/mutation of the proteins, developing therapeutic agents and improving treatment methods. The cells are useful for (a) elucidating signal transduction mechanism for cell ablesion through beta-catenin and plakoglobin, (c) elucidating signal transduction mechanism cross-reactivity of cadherin and desmosome cadherin, (d) elucidating function cells cates extendin in what signal transduction, (e) elucidating signal transduction of plakoglobin. The cells enable effective analysis of the transduction of plakoglobin. The cells enable effective analysis of the beta-catenin and plakoglobin. The sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New animal cell defective in or lacking expression of beta-catenin or plakoglobin, is useful for studying the function and regulation mechanism beta-catenin and/or plakoglobin, and in developing therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; prem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28198 BP; 6568 A; 7442 C; 7158 G; 7019 T; 0 U; 11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 28198;
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.rhes 46; Indels
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                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2; 41pp; Japanese
                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 2067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a mouse plakoglobin polynucleotide.
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                                           27-DEC-2001; 2001JP-00398640.
                                                                                         27-DEC-2001; 2001JP-00398640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.2.
Best Local 9; Conservative
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08-JUL-2003
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12-DEC-2001; 2001US-00021323.

07-SEP-2001

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Gaps

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HereK() PETKAN J.

PETK() FINGER T. E.

PRESC() FINGER T. E.

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Query Match
41.4%; Score 51.8; DB 13; Length 437;
Best Local Similarity 66.7%; Pred. No. 7.6;
Matches 74; Conservative 0; Mismatches 37; Indels 0; Gaps

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Search completed: November 9, 2005, 00:12:35 Job time : 104.246 secs

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Sequence 16, Appl
Sequence 188, App
Sequence 184, App
Sequence 1723, App
Sequence 1723, App
Sequence 17, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 1251, Appl
Sequence 1251, Appl
Sequence 1251, Appl
Sequence 1251, Appl
Sequence 1253, Appl
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Sequence 4150, Ap
Sequence 4138, Ap
Sequence 4138, Ap
Sequence 4140, Ap
Sequence 4145, Ap
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Sequence 12505, A
Sequence 14207, A
                                                                                                                                                                               8, 2005, 15:16:42; Search time 31.8505 Seconds (without alignments) 6421.701 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/RecTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-12505
US-09-128-155-16
US-09-128-155-16
US-09-107-433-2184
US-09-107-433-2184
US-09-107-433-184
US-09-107-433-1970
US-09-107-433-1970
US-09-107-433-1970
US-09-165-264-12
US-09-165-264-12
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US-09-165-264-13
US-09-165-264-13
US-09-949-016-12531
US-09-949-016-12720
US-09-949-016-13487
US-09-949-016-13487
US-09-949-016-13487
US-09-543-681A-41450
US-09-543-681A-41415
US-09-543-681A-4145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Maximum DB
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                                                                                                                                                                                      Run on:
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Sequence 24803, A Sequence 24804, A Sequence 67084, A Sequence 12084, A Sequence 12084, A Sequence 1271, A Sequence 16516, A Sequence 16777, A Sequence 1377, A Sequence 13719, A Sequence 1220, A Sequence 1280, A Sequence 12815, A Sequence 12915, A Sequence 12915, A Sequence 12915, A Sequence 12915, A Sequence 233, App Sequence 50, Appl Sequence 50, Appl Sequence 50, Appl	of Drosophila melanogaster	Length 865; Indels 0; Gaps 0; CCACCCCCAGCCGGCCCGC 60	ASSOCIATED OF DETECTION AND USES THEREOF
US-09-949-016-24803 US-09-949-016-67084 US-09-949-016-67084 US-09-949-016-12084 US-09-949-016-12084 US-09-949-016-12084 US-09-949-016-12077 US-09-949-016-12220 US-09-949-016-12220 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847 US-09-949-016-12847	roteins 57	42.1%; Score 52.6; DB 4; Length 865; conservative 0; Mismatches 34; Indels 0; Gaps cccrgcccrgcccraccccaccccaccccaccccacccc	6 KNOWN GENES SE, METHODS ,016
4 4 6 6 0 1 1 4 4 4 4 5 5 6 0 1 4 4 4 5 5 6 0 1 1 1 1 4 6 9 9 1 1 1 1 1 4 6 9 1 1 1 1 1 4 6 9 1 1 1 1 4 7 9 7 8 6 1 1 1 1 1 4 7 9 9 1 1 1 1 4 7 9 9 1 1 1 4 7 9 9 1 1 4 6 7 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 1 1 4 6 7 9 9 9 1 1 4 6 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	042 4 Application US/0927 3491 ATION: ATION: Nucleic acids B: File Reference: 73 CATION NUMBER: US/09/ G DATE: 1999-03-17 ED NOS: 62517 entin Ver. 2.0 2 ATION: n means any nu	11arity 68.2%; Pred. No Conservative 0; Misma CCTGCCCTGCCCTGCCCCCCCCCCCCCCCCCCCCCCCC	1-016-12505/c is 12505, Application US/09 No. 6812319 'INFORMATION'. Craig et a OF INVENTION' POLYMORPHISM OF INVENTION' WITH HUMAN USFERRNCE: CLO01307 IT APPLICATION WITH HUMAN IT APPLICATION WIMBER: US/0 IT APPLICATION NUMBER: 60/241 APPLICATION NUMBER: 60/241 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/231 FILING DATE: 2000-10-30 APPLICATION NUMBER: 60/231 FILING DATE: 2000-10-31 APPLICATION NUMBER: 60/231 FILING DATE: 2000-10-37 APPLICATION NUMBER: 60/231 FILING DATE: 2000-10-37
44444444444444444444444444444444444444	1-11 (1042 6702 (1042)		
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-270-76; Sequence 1) Patent No.; GRNERAL INN. APPLICANT; HILL OF 1 FILE REFER; CURRENT AL CURRENT AL CURRENT AL SOFTWARE:	Query Match Best Local S Matches 73 Qy 1 Db 159 Qy 61 Db 219	RESULT 2 US-09-94, Sequent; Sequent; GENETIC GENETIC TITLE TITLE TITLE TITLE TITLE TELE TELE

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US-09-128-155-16
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i Sequence 14207, Application US/09949016

i Patenn No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/291,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 20
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Pred. No. 0.071;
0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.1%; Score 51.4; DB 4; Length 670689; Best Local Similarity 67.0%; Pred. No. 0.071; Matches 73; Conservative 0; Mismatches 36; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCGCGCCGGCCCGGCTCGGCCCGACCCGGTTCCGCCGCGGCAGGC 115
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
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; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                             // NAME/KEY: misc_feature
// LOCATION: (1)...(670689)
// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12505
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; LOCATION: (1)...(670690)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14207
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Best Local Similarity 67.0%;
Matches 73; Conservative
                                SOFTWARE: FastSEC
SEQ ID NO 12505
LENGTH: 670689
                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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APPLICANT: ELIMBLES, ". ATMY
APPLICANT: ZHANG, YUAN
TITLE OF INVENTION: ANTISENSE COMPOSITIONS TARGETED TO BETA1-ADRENOCEPTOR-SPECIFIC MRI
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHOD OF USE
CURRENT APPLICATION NUMBER: US/09/614,034
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/152,717
PRIOR APPLICATION NUMBER: 09/152,717
PRIOR APPLICATION NUMBER: PT/US99/21007
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEC ID NOS: 204
SOFTWARE: Patentin version 3.0
SEC ID NO 188
LENGTH. 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21876 CNCCCCCCCCCCCCCCCCCCCCCCCCCCCCGNGCGGGCGCGCCCCC 21935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.5%; Score 50.6; DB 3; Length 152331; Best Local Similarity 66.4%; Pred. No. 0.12; Matches 71; Conservative 0; Mismatches 36; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%; Score 50.2; DB 4; Length 1845; 68.0%; Pred. No. 0.25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (1828)..(1828)
OTHER INFORMATION: WHERE N = A, T, C OR G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188, Application US/09614034 Patent No. 6489307 GENERAL INFORMATION:
APPLICANT: PHILLIPS, M. IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 68.03
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: UNKNOWN
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FOR DIAGNO

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                                                                     Sequence 185, Application US/09107433
| Patent No. 6800744
| GENERAL INFORMATION:
| APPLICANT: Lynn A Doucette-Stamm and David Bush
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
| SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
| THERAPBUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: CUNKNOWN COMPUTER: CUNKNOWN COMPUTER: CUNKNOWN CUNKRENT SOFTWARE: CUNKNOWN APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
PILING DATE: May 12, 1998
FILING DATE: July 2, 1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
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LOCATION: (B) LŌCATION 1...209
SEQUENCE DESCRIPTION: SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 100 Beaver Street
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LENGTH: 209 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
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Best Local Similarity 59.0
Matches 72; Conservative
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RESULT 7
US-09-107-433-185
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 0.39;
0; Mismatches 50; Indels
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ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
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APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/085131
APPLICATION NUMBER: 60/05153
ATTORNEY/AGENT INFORMATION:
NAME: ATIALALLO PAMELER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECHONE: (781,893-5007)
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COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                             US-09-107-433-2184/c
; Sequence 2184, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 2184:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
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59.0%;
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Best Local Similarity 59.0
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
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                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENY PELCATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
ATTORNEY/AGENT INFORMATION:
MAME: ALIANG DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...308; SEQUENCE DESCRIPTION: SEQ ID NO: 1723: US-09-107-433-1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1970, Application US/09107433; Patent No. 6800744; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 308 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 1723:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
Patent No. 6800744
GENERAL INFORMATION:
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US-09-107-433-1970/c
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
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                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
MEDIUM TYPE: CD/ROM
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: 30-Unn-1998
APPLICATION NUMBER: 60/085131
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: JUN 2, 1997
ATTORNEY/AGENT INFORMATION:
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; LOCATION: (B) LOCATION 1...282

; SEQUENCE DESCRIPTION: SEQ ID NO: 184:

US-09-107-433-184
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                                   Sequence 184, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 100 Beaver Street
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 59.0%
Then 72; Conservative
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ORIGINAL SOURCE:
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US-09-107-433-184
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                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Primer sequence US-09-165-264-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 320;
                                                                                                                                                                                                                                                                      39.7%; Score 49.6; DB 3; Length 3 67.3%; Pred. No. 0.4; Live 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       64 CGCCCCCGCGCCCGGCTCGGCCCGACCCGGTTCCGCCGC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09165264
Fatent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagemoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION UNDER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 12
LENGTH: 318
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Sequence 8, Application US/09165264

Patent No. 6197510

GENERAL INCOMMITION:

APPLICANT: Vinayagamoorthy, Thuraiayah

TITLE OF INVENTION:

FILE REPERENCE: 44747

CURRENT APPLICATION NUMBER: US/09/165,264

CURRENT APPLICATION NUMBER: 1998-10-01

NUMBER OF SEQ ID NOS: 14
                     CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
LENGTH: 320
                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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SEQ ID NO 8
LENGTH: 319
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 67.33
Best Local Similarity 67.33
Conservative
          44747
        FILE REFERENCE:
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                                                FOR DIAGNO
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCCCTGCCCTGCCCCTGCCCCCACCCCCAACCCCCAACCCCCAGCCGGCGCCCGC
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                                                                                                                         ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09165264
; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
; APPLICANT: VIANY@amoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM 1809660
COMPUTER: CD/ROM 1809660
COMPUTER: CD/ROM 1809660
COMPUTER: CD/ROM 1809660
COMPUTER: CD/ROM 1809660
COMPUTER: CD/ROM 1809660
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
ATTORNEY/AGENT INFORMATION:
NAME: ARIGISERATION:
NAME: ARIGISERATION NUMBER: 40,489
REGISERRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature

LOCATION: (B) LŌCATION 1...612

; SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

US-09-107-433-1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1970;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                   NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
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Best Local Similarity
....has 72; Conservat
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ORIGINAL SOURCE:
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US-09-165-264-11/c
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8
                                                                                                                                                                                    Gaps
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                                                                                                                                   Query Match 39.5%; Score 49.4; DB 3; Length 319; Best Local Similarity 66.4%; Pred. No. 0.43; Matches 71; Conservative 0; Mismatches 36; Indels (
                                                                                                                                                                                                                                                                                                                   61 GCCCGCCCCGCGCGGGCCCGGCTCGGCCCGACCCGGTTCCGCCGC 107
                                                                                                                                                                                                                                                                                                                                                             Query Match 39.5%; Score 49.4; DB 3; Length 320; Best Local Similarity 66.4%; Pred. No. 0.43; Matches 71; Conservative 0; Mismatches 36; Indels (
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US-09-165-264-7/C

| US-09-165-264-7/C

| Sequence 7, Application US/09165264
| Patent No. 6197510
| GENERAL INFORMATION:
| APPLICANT: Vinayagamoorthy, Thuraiayah
| TITLE OF INVENTION: Multi-Loci Genomic Analysis
| FILE REFERENCE: 44747
| CURRENT APPLICATION NUMBER: US/09/165,264
| CURRENT APPLICATION NUMBER: US/09/165,264
| CURRENT PILING DATE: 1998-10-01
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO. | LENGTH: 320
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Fatent No. 6197510
GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT PILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 320
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-165-264-13/c
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39.5%; Score 49.4; DB 3; Length 320;

Query Match

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0; Gaps
                                                                              Best Local Similarity 66.4%; Pred. No. 0.43;
Matches 71; Conservative 0; Mismatches 36; Indels
                                                                                                                                    Search completed: November 8, 2005, 19:52:44 Job time : 33.8505 secs
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Sequence 65924, A
Sequence 17653, A
Sequence 5998, Ap
Sequence 3757, Ap
                                                                                                                                                                         8, 2005, 18:06:53 ; Search time 161.744 Seconds (without alignments) 6391.142 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Cgn2_6/ptodata1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO6_Wish_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO6_Wish_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_RIW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO9_RIW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO0_RIW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO0_RIW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO0_RIW_PUB.seq:*
| cgn2_6/ptodata1/pubpna/USO0_RIW_PUBCOMB.seq:*
| cgn2_6/ptodata1/pubpna/USO0_RIW_PUB.seq:*
| cgn2_6/ptodata
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
5.1.6
Compugen Ltd
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US-10-425-115-65924
US-10-425-115-17653
US-10-021-323-5998
US-10-437-963-3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9794790 seqs, 4134909567 residues
GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                               November
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Perfect score:
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88435, Ap
269876, A
269876, A
215390, A
315390, A
315390, A
5654, Ap
63819, A
63819, A
9291, A
9291, A
64501, A
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8767, Ap
133228,
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11145, A
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14077, A
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131885,
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106153,
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133788,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56975_1
US-10-767-701-8805
US-10-767-701-8435
US-10-425-115-82176
US-10-424-519-82176
US-10-424-519-821316
US-10-424-519-821316
US-10-027-623-31508
US-10-027-623-31508
US-10-027-623-31508
US-10-767-701-5654
US-10-425-115-93481
US-10-425-115-93819
US-10-425-115-913811
US-10-425-115-913811
US-10-425-115-1145
US-10-425-115-1145
US-10-425-115-1145
US-10-425-115-118311
US-10-425-115-118311
US-10-425-115-11831328
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US-10-424-599-107958
US-10-739-930-4713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.4°
Matches 83; Conservative
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ORGANISM: Sorghum bicolor
 533.4.6.5
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                                                                                                                                  ) OTHER INFORMATION: Clone ID: MRT4577_116102C.1 US-10-425-115-17653
                                         NAME/KEY: unsure
LOCATION: (1)..(972)
OTHER INFORMATION: unsure at all n locations
    ORGANISM: Zea mays
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                                                                                                               FEATURE:
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US-10-425-115-17653, Application US/10425115

Sequence 17653, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 17653

LENGTH: 972
                                                                                                                                                                                                                                                              WS-10-425-115-65924

Sequence 65924, Application US/10425115
Publication No. US20040214272A1

Sequence 65924, Application US/10425115

Publication No. US20040214272A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules

TITLE OF INVENTION: Nucleic Acid Molecules

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 65924
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                                            61 GCCCGCCCCCCGCCCCGGCCCCGGCCCGACCCGGTTCCGCCGGCGGGGAGCGGGGGGGC 120
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1 CCCTGCCCCTGCCCCTGCCCCCACCCCACCCCCACCCCCACCCCCAGCCGGCGCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_160123C.1
US-10-425-115-65924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(737)
OTHER INFORMATION: unsure at all n locations
PERATURE:
                                                                                                                                    121 CCAGC 125
                                                                                                                                                                              302 GGGGC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     678 CC 679
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APPLICANT: Feng, Faul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Siegler, Todd E.
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 5998
LENGHH 420
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; OTHER INFORMATION: Clone ID: LIB3828-011-Q1-N6-H6
US-10-021-323-5998
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Sequence 3757, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: Royalic, David K.

APPLICANT: Royalic, David K.

APPLICANT: Cao, Yohua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-021-323-5998/c; Sequence 5998, Application US/10021323; Publication No. US20040123340A1; GENERAL INFORMATION:
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US-115-82176

US-10-425-115-82176

Sequence 82176, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 82176
LENGTH: 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBURE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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44.5%; Score 55.6; DB 19; Length EBst Local Similarity 63.2%; Pred. No. 0.0002;
Matches 79; Conservative 0; Mismatches 46; Indels
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US-10-424-599-26988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 44.6%; Score 55.8; DB 21; Best Local Similarity 70.1%; Pred. No. 0.00018; Matches 75; Conservative 0; Mismatches 32;
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OTHER INFORMATION: unsure at all n locations
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 26988, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-26988/c
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LENGTH: 809
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                                           APPLICANT: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Li, Ping Title OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8435, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Evovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: NUCleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUCLEIC Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/767,701
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 668;
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44.8%; Score 56; DB 20; Length 678;
Best Local Similarity 68.8%; Pred. No. 0.00017;
Matches 77; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS39772_1
US-10-767-701-8435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 56.2; DB 20;
Best Local Similarity 65.6%; Pred. No. 0.00015;
Matches 82; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT4530_10702C.1

US-10-437-963-3757
                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(668)
OTHER INFORMATION: unsure at all n locations
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CCAGC 125
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US-10-767-701-8435
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US-IU-UZ/-51Z-11-UZ/
Sequence 13508, Application US/10027632
Publication No. US20030204075A9
Publication No. US20030204075A9
FUBLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR PRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 2000-03-29
FRIOR PELING DATE: 1999-09-28
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FRIOR FILING DATE: 1999-09-08
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44.2%; Score 55.2; DB 18;
Best Local Similarity 69.2%; Pred. No. 0.00023;
Matches 72; Conservative 0; Mismatches 32;
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 31508
LENGTH: 956
                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1) ... (956); OTHER INFORMATION: n = A,T,C or G US-10-027-632-31508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(956)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-31508
                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(956)
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                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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LENGTH: 956
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                                                                                                                                                                                                                                                                                                      Sequence 28390, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brazauk, Brad
; APPLICANT: Brazauk, Brad
; APPLICANT: Brazauk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)8
; CURRENT APPLICATION NUMBER: US/10/437,963
; SEQ ID NOS: 204966
; SEQ ID NOS: 204966
; SEQ ID NOS: 204966
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   1 CCCCTGCCCCTGCCCCTGCCCCCACCCCCACCCCCACCCCCACCCCCAGCCGGCGCCCGC 60
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR PILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PILING DATE: 10000-03-29
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
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44.3%; Score 55.4; DB 20; Length
Best Local Similarity 69.2%; Pred. No. 0.00021;
Matches 74; Conservative 0; Mismatches 33; Indels
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US-10-437-963-28390
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LOCATION: (1)..(862)
OTHER INFORMATION: ungure at all n locations
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Publication No. US20020198371A1
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                                                                                                CCAGC 125
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; Sequence 39481, Application US/10425115
; Sequence 39481, Application US/10425115
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cano, Yongue
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 93481
LENGTH: 581
                                                                                                                                                                                                                                                                                       Sequence 5654, Application US/10767701

Sequence 5654, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILER REFERENCE: 38-21 (55535) B
CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 5654

LENGTH: 713
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US-10-767-701-5654
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US-10-425-115-93481
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LOCATION: (1)..(581)
OTHER INFORMATION: unsure at all n locations
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US-10-425-115-93481
                                                                                                                                                                                                                            RESULT 12
US-10-767-701-5654
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Sequence 9291, Application US/10767701
Subblication No. US20040172684A1
GENERAL INFORMATION
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 9291
LENGTH: 793
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE SPERENCE: 38-21(5)222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 63819
LENGTH: 788
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US-10-767-701-9291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.8%; Score 54.8; DB 20; Best Local Similarity 67.5%; Pred. No. 0.0003; Matches 77; Conservative 0; Mismatches 37;
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US-10-425-115-63819
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OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 63819, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Sorghum bicolor
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ORGANISM: Zea mays
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NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-425-115-63819
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Search completed: November 8, 2005, 23:53:29 Job time : 162.744 secs

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BRY 4732 Anopheles 963070A02

SAIL 618 Drosophil

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Pan trogl AGENCOURT

OM nucleic

Run on:

Sequence:

Searched:

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Confact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-38618
Fax: (206) 616-38618
Email: jwallacedu.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 4832 row: B column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 821.
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1 (bases 1 to 821)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Holzman, T., Feller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ893474 15.2 A2 C06_T7A CIT Approved Human Genomic Sperm Library D Homo Bapiens genomic clone Plate=4832 Col=12 Row=E, genomic survey
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
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/mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=4832 Col=12 Row=E"
                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .821
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                          BQ608819
CNS01HTD
BF866526
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GSS.
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AUTHORS
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ORIGIN
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AG435406 MNE muscu
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EE51555 hx97f12.x
CR62226 full-leng
BQ708087 AGENCOURT
CL078342 CH216-149
AL059666 Drosophil
AL185299 Tetraodon
CL475036 SAIL_230_AG334095 MNE muscu
AL064031 Drosophil
BQ651163 AGENCOURT
AG643467 Pan trogl
AL104949 Drosophil
BL1649457 SAIK_0159
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CL500140 SAIL 679
AG331885 MNB muscu
CL492395 SAIL 566
BQ952554 AGENCOURT
BU148615 AGENCOURT
CL468510 SAIL 1287
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              5.1.6
Compugen Ltd.
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              GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                               nucleic search, using sw model
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BU148615
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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gb_est2:*
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Minimum I Maximum I

Database

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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Amphibia; Ranopus.

1 (bases 1 to 982)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A7 Bethesda, MD 20892
Email: cgapbe-r@mail.nih.gov
Tissue Procurement:
                                                                                                                                                                                                                                                                                               UJZJ933
AGENCOURT 14164463 NICHD_XGC_Brn1 Xenopus laevis cDNA clone
IMAGE:6551625 5', mRNA sequence.
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/note="Grgan: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) libzary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               con Library Preparation: Life Technologies, Inc.
con Library Preparation: Life Technologies, Inc.
con Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM4570 row: p column: 24
High quality sequence stop: 297.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6951625"
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Mus musculus molossinus DNA, clone:MSMg01-313H22.T7, genomic survey
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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BAC end Sequences of Library MSMg01
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51.5%; Score 64.4; DB 9; Length 1283;
Best Local Similarity 70.5%; Pred. No. 0.065;
Matches 86; Conservative 0; Mismatches 36; Indels 0
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/clone_lib="MSMg01 Mouse Male BAC Library"
Score 65, DB 8; Length 821;
Pred. No. 0.056;
0, Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                        61 GCCGCCCCGCGCGCCCCGGCTCGGCCCGGACCCGGGTTCCGCC 105
                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-313H22.T7"
/sex="male"
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AGENCOURT_8475084 NIH_MGC_113 Homo sapiens cDNA.clone IMAGE:6301404 BQ708087
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 996)
                              Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Gruber, Orassee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                              Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/db_xref="taxon:9606"
/clone="CSODC004Y008"
/clabue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Pred. No. 0.13;
0; Mismatches 1; Indels 0.
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98.4%;
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/lab_host="DR10B"
/lab_host="DR10B"
/clone_lib="NCI_CGAP_GC6"
/note="Vector: pT713-Pac (Pharmacia) with a modified
note="Vector: pT713-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP_GC4 was prepared, and
sf circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
this DNA was used as tracer in a subtractive hybridization
caction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonelDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL, send email to:
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
hx97f12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3195791 3' similar to contains element MSR1 repetitive element ;, mRNA
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CR622226
CR622226.1 GI:50503033
HTC; CNSLT_CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 63.2; DB 2; Length 425; 68.8%; Pred. No. 0.13; ive 0; Mismatches 39; Indel8
                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infowingge.llnl.gov
Seg primer: -40UP from Gibco
High quality sequence stop: 206.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3195791"
                                                                                      BE551555
BE551555.1 GI:9793338
                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                                                                                        Homo sapiens
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Matches 86; Conserv
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FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopua; Silurana.

E. 1 (bases 1 to 1674)

S. Kremtzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

L Ontact: Richard K Wilson

Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH216-149D22_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-149D22, genomic survey sequence. CL078342
Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 bb. Constructed by J. Wang (Reesarch Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/noce="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                  DB 6; Length 1024;
                                                                                                                                                                                                                              Query Match 49.6%; Score 62; DB 6; Length 102
Best Local Similarity 68.6%; Pred. No. 0.17;
Matches 83; Conservative 0; Mismatches 38; Indels
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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-149D22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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High quality sequence start: 300
High quality sequence stop: 387.
Location/Qualiflers
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                                                                                         1. 11024
| Organism="Danio rerio"
| Organism="Danio rerio"
| Ab xref="taxon.7955" |
| Clone="IMAGE:6803474" |
| / tissue_type="embry108 (T1-resistant)" |
| / tab host="Danio (T1-resistant)" |
| / clone | 11b="NCI_CGAP_ZEmb3" |
| / clone | 12b="NCI_CGAP_ZEmb3" |
| / clone | 12b="CGAP_ZEmb3" |
| / clone | 12b="
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1 (Spriniformes, Cyprinidae, Danio.

1 (Danses 1 to 1024)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Chi-Bin Chien
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.B. Consortium/Link at:

http://image.llnl.gov h column: 01

High quality sequence start: 40

High quality sequence stop: 419.
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                                    'organism="Homo sapiens"
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TITLE JOURNAL AUTHORS

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Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 01-APR-2004
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                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodontidae, Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bouneau, L., Fisher, C.,
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigrovitidis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/note="Genoscope sequence ID : COAG243DE06SP1-end
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Arabidopsis thaliana (thale cress)
                            GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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          AL185299.1 GI:7823403
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, nb wsp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                          B43 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
ELY), genomic survey sequence.
ALO59666
ALO59666.1 GI:4947129
GSS.
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 243J12 of library G from Tetraodon nigroviridis, genomic survey
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/note="end : TET3"
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are derived from the mouse BAC library MSMg01. For BAC
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                                                                                                                e-mail: abe@rtc.riken.jp
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Syngeric Blotechnology Inc.
Syngeric Blotechnology Inc.
Brail: allen.sessions@syngenta.com
ABRC Stock Number CS810670; T-DNA left border flanking sequences of Syngeric Arabidopsis Insertion Library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not single contiguous sequences.
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Direct Submission
Direct Submission
Submitted (17-NOV-2003) Massahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehhro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@qsc.riken.jp, UR:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
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Mus musculus molossinus DNA, clone:MSMg01-124N12.TJ, genomic survey
                 Sessions, A., Burke, E., Presting, G., Aux, G., McElver, J., Patton, D., Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J.D., Cotton, D., Ballis, D., Snell, J., Miguel, T., Hutchison, D., Kimmerly, B., Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S.A. A high-throughput Arabidopsis reverse genetics system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus molossinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
/clone="5AIL_230_F07.v1"
/clone="5AIL_Collection"
/note="T-NA left border sequences were isolated using
modified TAIL-PCR strategy"
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/ecotype="Columbia"
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Week jenoscope.come interest in the project of a collaboration of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Goosgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism≃"Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/sub_species="molossinus"
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/sex="male"
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@qsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG043467 840 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-021M16.F, genomic survey sequence.
AG043467
   of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                          61 GCCCGCCCCCCGCCCGGGCCCGGCTCGGCCCGACCCGGTTCCGCCGCGGGCAGGCGGGGC 120
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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/db_xref="taxon:9598"
/clone="PTB-021M16.F"
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R.Site 2 : Sari
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/mol type="makka"
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AGENCOURT_8488514 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6296195
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 1134)
NIH-MGC http://mgc.nci.nih.gov/.
Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Contact: Robert Straubberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LiCM2503 row: k column: 12
High quality sequence start: 17
High quality sequence stop: 135.
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/mol_type="genomic DNA"
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/clone="BARC13L17"
/clone lib="RRC1-98"
                                                                                                                                                                                                                                                                                                                                                                                                                       48.6%; Score 60.8; DB llarity 66.4%; Pred. No. 0.28; Conservative 2; Mismatches
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/organism="Homo sapiens"
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121 CÇAG 124
                424 GCCG 421
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AC093174 135675 bp DNA linear PRI 08-NOV-2002 Homo sapiens chromosome 3 clone RP11-167M22 map 3p, complete AC093174. HTG9. Homo sapiens (human) Homo sapiens (human)	Mammalia; Butherla; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 135675) Wu, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Bing, H., Dong, W., Pan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, J., Wang, L., Wang, K., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Zang, Y., Zhang, X., Zhang, H., Zhang, L., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.,	Chromosome Jang, Fr. Chromosome Jang, Fr. Chages I to 13575) Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Bao, J., Bao, Q., Bao, W., Bian, X., Gan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, F., Li, G., Li, J., Li, Li, Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, W., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, J., Wang, J., Wang, L., Wang, L., Wang, X., Wang, X., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Zhang, X., Zhang, M., Zhang, H., Zhang, Y., Zhang, X., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N.	Yu,J. and Yang,H. Direct Submission Submitted (13-AUG-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China
RESULT 1 AC093174 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL

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12128 GTGTCATCTAGAATGAAGTTATATTTACTAAGGATCGTTTTTGCCATGTATAACTTCTC 42187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACATTAACTTTCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTCTTAAGTCTGTGCA
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3 (bases 1 to 135675)
Wu, Q., Bao, J., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, O., Gu, X., Guo, D.,
Guo, Z., He, L., Hu, S., Hanng, F., Jin, Y., Kang, N., Li, C., Li, C.,
Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, N.,
Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Qi, Y., Song, E.,
Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Wang, H., Wang, J.,
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Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X.,
Zhang, X., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J., and
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator B1G Dye; 45% of reads
Chemistry: Dye-terminator B1G Dye; 45% of reads
Chemistry: Dye-terminator B1G Dye; 45% of reads
Consensus quality: 0 bases at least Q40
Consensus quality: 0 bases at least Q30
Consensus quality: 6 bases at least Q20
Insert B12: 3392; sum-of-contigs
Quality coverage: 0.00x in Q20 bases;sum-of-contigs
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http://www.genomics.org.cn
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/rj variation 14	/rej variation 252 /fr	repeat_region 357	variation 7.pg 374 /fre	/rorrepeat_region 433	/ri variation 15	/f: /ro misc feature 177	G	/rj /rj repeat_region 20			14 Q.	gamm variation 2076 /gen	/r: /ro variation 210		variation 21	/rep variation 2382		variation 24 /g /f:	/r variation 24	יייי איניי	variation 30	/r//r///r///r/////////////////////////	₩	variation 33	

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22493. .2251
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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, J., Castler, A., Catlymore, A., Cooke, P., Catlymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Garath, G., Hagos, B., Haedrod, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGrran, K., McLaughlin, J., Melfrim, J., Peterson, R., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stanger-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                              162388 TTTTAAAAGATTCTCCAGCCCTGCATGATTTATGATGAATCATTTTGTGGTCTGTTAGTT 162447
                                                                                                                                                                                                                                                                                                          AC015995 221402 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 3 clone RP11-33519 map 3, WORKING DRAFT SEQUENCE, 36 unordered pieces.
                                                                                                                                                                                                      162568 GTACACATTCTGAACATGTGTGTATATTGAAAATCTTGTCTCTTTTTTATTGTTAAG 162624
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 221402)
                                                                                                                                                                                   661 AATAGAGAAAGTTAAATTTAGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 3, clone RP11-33519
                                                                                                                                                                                                                                                                                                                                                                                  ACOIS995.5 GI:9966961
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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Length 180963;
                                                                                                                                                                               Sequencing vector: pUC18; 100% of reads Chemistry: Dye-terminator: ET 53% of reads Chemistry: Dye-terminator: ET 53% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 369 bases at least Q40 Consensus quality: 751 bases at least Q30 Consensus quality: 755 bases at least Q20 Insert size: 773; sum-of-contigs Quality coverage: 1.48x in Q20 bases;sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                        Center project name:1% project
Center clone name: RP11-33519
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                     Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/clone="RP11-33519"
                                                        Center code:Beijing
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2: contig of 2455 bp in length
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                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                              2.51630941286114Chemistry: Dye-terminator Big Dye; 100% of
                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a working draft, sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                 On Sep 5, 2000 this sequence version replaced gi:7329342. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                  reads
                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project_Information
Center project name: 12392
Center clone name: 335_I_9
                                                                                                                                                                                                                                                                                                                                                  Insert size: 182000; agarose-fp
Insert size: 217902; sum-of-contigs
Quality coverage: 6.0 in Q20 bases; agarose-fp
Quality cov.
                                                                                                                                                                                                  Assembly program: Phrap, version 0.960731
Consensus quality: 188096 bases at least Q40
Consensus quality: 198983 bases at least Q30
Consensus quality: 206638 bases at least Q30
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product="peroxisome proliferator-activated receptor gamma"
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               Arterioscler. Thromb. Vasc. Biol. (2003) in press
2 (bases 1 to 851)
Marihaeqhe,A., Fajas,L., Helbecque,N., Auwerx,J. and Amouyel,P.
Direct Submission
Submitted (23-SEP-2002) INSERM U508, Institut Pasteur de Lille,
rue du Pr Calmette - BP 245, Lille 59019, France
Location/Qualifiers
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Matches 769; Conservative
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1 (Dases 1 to 851)

Meirhaeghe,A., Fall, Gouilleux,F., Cottel,D., Helbecque,N., Auwerx,J. and Amouyel,P.

A functional polymorphism in a STATSB site of the human PPAR gamma 3 gene promoter affects height and lipid metabolism in a French
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                                                   1 TCATGTAGGTAAGACTGTGTAGAATGTCGGGTCTCGATGTTGGCGCTATTCAAGCCCTGA
                                                                        98593 TCATGTAGGTAAGACTGTGGGGTGTGGGGTCTCGATGTTGGCGCTATTCAAGCCCTGA
                                                                                                                  61 TGATAAGGCTTTTGGCATTAGATGCTGTTTTGTCTTCATGGAAAATACAGCTATTCTAGG
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99.1%; Pred. No. 6.1e-160; tive 0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-OCT-2004) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
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ACISIB49. I GI:53983836
HTG; HTGS PHASE2, HTGS DRAFT.
Callithrix jacchus (white-tufted-ear marmoset)
Callithrix jacchus
Callithrix jacchus
Eukaryota, Metazoa; Oprofate; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
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GTGATGGAAATAGGAAAGTAGGTGAAGTGAATCTAATAGATGTTTCTTTTATGAAATAAT
                                   TTTTAAAAGATTGTCCAGCCCTGCATGATTATGATGAATCATTTTGTGGTCTGTTAGTT
                                                                                                    ACTITIAGAGAATAGAAAGCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be
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(allithrix.

(bases I. (bases I. o. 186028)

Cheng, J., F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.

Direct Submission

Unpublished
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: Plasmid; pUC18
Chemiatry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.

* NOTE: This is a "working draft' sequence. It currently

* consists of 2 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=PPARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Funding agent: Programs for Genomic Applications (NHLBI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           paired
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id (http://baboon.math.berkeley.edu/mavid) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Produced by Berkeley PGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: J108-42F14
Bac Clone Name: CH259-42F14
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provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 26679; contig of 26679 bp in length
2679; app of unknown length
26780 186028; contig of 159249 bp in length.
                                                                                                                                                                                                                                                                                                                                  Length 186028;
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                                                                                                                                                                                                                                                                                                                                  Score 565.4; DB 2;
Pred. No. 1.8e-115;
                                                                                                                                                    Location/Qualifiers
1. .186028
//organism="Callithrix jacchus"
/mol_type="genomic DNA"
/db xref="taxon:948"
/clone="CH259-42F14"
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Matches 663; Conservative
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sequencing reads that have not been assembled into
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KRESEACH, 320 Charles Street, Cambridge, MA 02141, USA
Barran, N. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazer, B., Choepel, Y., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreita, P., FitGerald, M., Gage, D., Galagan, J.,
Gardyan, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hangos, B.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Machous, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Kaise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Severy, P.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Yesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Limer, Sumitted (10-007-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 10, 2002 this sequence version replaced gi:23592138.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.wanhington.edu/RM/RepeatMasker.html
  Homo sapiens chromosome 17 clone RP11-1200B1 map 17, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 65160)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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Homo sapiens chromosome 17, clone RP11-1200B1
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                                                                                                         AC135179.2 GI:23683246
HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                           Unpublished
                                          DEFINITION
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AUTHORS
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved. 100 bp of 100 bp of 727 bp in length 100 bp of 719 bp in length 100 bp of 718 bp in length 100 bp of 719 bp in length 100 bp of 732 bp in length of 732 bp in length of 732 bp in length 100 bp of 718 bp in length 100 bp of 723 bp in length of 703 bp in length of 702 bp in length 720 bp in length in length in length bp in length in length in length bp in length in length in length in length in length in length in length in length in length bp in length in length in length in length in length in length in length bp in length ,05 of 20 of 701 bp 17 100 bp 786 br 100 bp of 719 bp i 100 bp of 717 bp i 100 bp of 741 bp i 100 bp 100 bp of 727 bp 100 bp of 717 bp : ď ď 734 bp ď đ ф ď đq ф ďq ď 100 bp of 731 1 100 bp of 735 1 100 bp of 724 l of 712 | 100 bp of 722 | 100 bp of 704 100 bp of 709 100 bp of 715 100 bp of 721 100 bp of 722 100 bp of 607 728 100 bp of 729 100 bp of 731 100 bp contig gap of 1 contig gap of 1 contig gap of contig gap of contig gob of contig gap of gap of contig gap of contig gap of contig gap of contig gap of contig gap of gap of gap of gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of gap of contig gap of gap of contig gap of gap of contig gap of contig gap of contig gap of contig contig contig gap of gap of gap of gap of gap of 720: 25397: 25497: 26104: 1624: 4038: 13991: 4869: 5804: 6638: 23844: 4969: 14814: 15516: 8888: .9729: 23022: 9066 12364: 13073: 17252:

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                                                                                                                                                                                                                                                         AC131898 212216 bp DNA linear HTG 27-AUG-2002
Oryctolagus cuniculus clone LB1-83M7, WORKING DRAFT SEQUENCE, 12
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-AUG-2002) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
Draft Sequence Produced by Berkeley PGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 212216)
Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M. and Cheng,J.-F.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
1 (bases 1 to 212216)
    33933 TGGAAAGCAAACATTCAGAATGAAATCCAATAGAGAAGGTAAATTTTATTTTGGGCATGTAC
                                                                                                                                                       ATTITGGCAGCCTAGGCTGTACATGTGTACACATTCTGAACATGTGTGTATATTGAAA
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http://pga.lbl.gov/cgi-bin/search_cvcgd?type=nkvalue=PPARG
Funding agent: Programs for Genomic Applications (NHLBI)
Contact: 'Joga.lbl.gov/cgi-bin/search_cvcgd?type=nkvalue=PPARG
Funding agent: Programs for Genomic Applications (NHLBI)
Contact: Jogy Schwartz' jrschwartz@blb.gov
if library name is LBI to LB4, please see website
for a description: http://www-gsd.lbl.gov/cheng/BAC.html
Summary Statistics:
Sequencing vector: Plasmid; pUC18
Chenistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
to not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
trus of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., and Cheng,J.-F.
Direct Submission
Unpublished
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gap of unknown length
contig of 2066 bp in length
gap of unknown length
contig of 4520 bp in length
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Center Code: PGABERK
Center Project Name: R052-83M7
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HTG; HTGS PHASB1; HTGS DRAFT.
Oryccolagus cuniculus (rabbit)
Oryctolagus cuniculus
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| of 710 bp in length
| 100 bp
| of 732 bp in length
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1 of 719 bp in length

1 00 bp in length

1 100 bp in length

2 of 722 bp in length

2 100 bp

3 of 720 bp in length
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g of 710 bp in length
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g of 705 bp in length

g of 739 bp in length

f 100 bp

f 100 bp

f 100 bp in length

f 100 bp in length

g of 728 bp in length

g of 718 bp in length
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Sizemen B. Nusbaun, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaun, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Diaz, J. S., Dodge, S., Paro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liudblad-Toh, K., Marchar, J., Marchan, J., Marchan, J., Marchan, J., Marchan, J., Marchan, J., Marchan, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M., Wiman, D., Young, G., Zainoun, J., Direct Submission
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 6, 2004 this sequence version replaced gi:29029334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                            Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 6, clone RP24-507D15
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is gap of unknown length
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contig of 8449 bp in length
gap of unknown length
contig of 12795 bp in length
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contig of 14010 bp in length
contig of 14048 bp in length
contig of 19448 bp in length
contig of 19448 bp in length
gap of unknown length
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Pred. No. 4.8e-19;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                contig of 26880 bp in length
gap of unknown length
contig of 67959 bp in length.
                                                                                                                                                                                                                 contig of 23650 bp in length
gap of unknown length
contig of 25686 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"
/clone="LB1-83M7"
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371 TTTCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTTCTTAAGTCTGTGCAGTAATAGAGG 430
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Mutzhy, D.Marie., Matzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranalke, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 185737;
                                                                                                                                                  1 54649: contig of 54649 bp in length 0 54149: gap of 100 bp 0 156594: contig of 101845 bp in length 5 156694: gap of 100 bp 5 186737: contig of 29043 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.3%; Score 103.6; DB 2; Length 1 Best Local Similarity 57.7%; Pred. No. 4.8e-13; Matches 225; Conservative 0; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-24 Male Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="RP24-507D15"
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Center: Genome Center
Center: Baylor College of Medicine
Center: BCM
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Rat Genome Sequencing Consortium.
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                                                                                                                                       Murny D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S. L., Amaratunge, H.C., Are, J. R., Ayele, M., Banks, T., Barbaria, J., Bondan, C., Adio-Oduola, B., Ali-osman, F.R., Baryant, N. Barbaria, J., Bancon, J., Briede, M., Brown, B., Baryant, N. B., Barbaria, J., Boude, S., Briede, M., Brown, R., Brown, M., Baryant, N. Bancon, J., Bancon, J., Barden, C., Burrell, K.L., Burch, C., Burch, P., Burch, P., Burkett, C., Burrell, K.L., Burden, C., Chavez, D., Chance, J., Cowde, M. D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Elbaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C., Hawe, S., Hamalton, K., Harrandez, O., Hadgson, A., Hayer, M., Halloway, C., Halling, B., Hommai, P., Howard, S., Huber, J., Hulyk, S., Hume, J., Jacobson, L. B., Jacobson, B., Jair, Y. Johnson, R., Johlive, S., Joudh, S., Karlson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, M., Mapus, P., Martin, R., Martin, C., Liu, J., Liu, M., Maul, D., Newtson, N., Nickerson, B., Nachton, G., Mincer, S., Mitchell, T., Mohabbat, R., Morgan, M., Nayuen, N., Nickerson, E., Nached, M. P., Mohabbat, R., Mohabbat, R., Mohabbat, R., Mohal, D., Newtson, J., Raven, S., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Burn, H., Shooshtari, N., Sisson, I., Sodergren, S., Scott, G., Walliame, G., Walliame, G., Walliame, G., Walliame, S., Warren, R., Walli, S., Warren, R., Walliame, S., Warren, R., Walli, R., Walliame, 
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:22855703.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table bellow represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold'). Within each contig-scaffold by sized gaps filled with Ns to the estimated and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
Rattus norvegicus (Norway rat)
Rattus norvegicus
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DEFINITION Rattus norvegicus clone CH230-24K10, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
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Assembly program: Phrap, version 0.990329
Consensus quality: 220652 bases at least Q40
Consensus quality: 223895 bases at least Q30
Consensus quality: 225929 bases at least Q30
Consensus quality: 225929 bases at least Q20
Estimated insert size: 229375; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 245724: contig of 245724 bp in length.
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                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: TUQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 88.6; DB 2;
60.7%; Pred. No. 9.8e-10;
live 0; Mismatches 109;
Center: Baylor College of Medicine
Center code: BCM
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/db_xref="taxon:10116"
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243338. .245724
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/note="wgs_contig"
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Best Local Similarity 60.77
Matches 184; Conservative
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           COMMENT
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                                                                                                                                                                                                                                                                               Narany, Dearle, Netzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anyalaebachi, V., Anguiano, D., Anyalaebachi, V., Anguiano, D., Anyalaebachi, V., Anguiano, D., Anyalaebachi, V., Baladrain, Bandarani, S., Amin, A., Anguiano, D., Bandaranike, D., Barber, M., Barneted, M., Benahmed, F., Biswalo, K., Blayi, T., Blanker, D., Barneted, M., Encher, A., Cardenas, V., Carter, K., Cardenas, C., Ding, Y., Durh, H., Duyan, R., Chen, G., Chen, R., Chen, Y., Chen, S., Chen, Y., Cardenas, V., Carter, K., Cardenas, S., Dunn, A., Durbin, K., Duval, B., Baves, V., Baraer, C., Darae, C., Ding, Y., Carter, P., Durandaz, S., Filhy, M., Flagg, N., Porbes, L., Poster, M., Gebregocrgis, B., Gerr, K., Galisi, A., Garte, M., Garra, M., Gabisi, A., Garte, M., Garra, M., Gabisi, A., Garte, M., Garra, M., Harandaz, S., Filhy, M., Flayin, N., Flayin, M., Handerson, M., Handis, D., Jackson, A., Handerson, N., Harnandaz, R., Haves, A., Handerson, N., Harnandaz, R., Haves, A., Handerson, N., Harnandaz, M., Haves, A., Handerson, N., Harnandaz, R., Kath, Y., Kath, Y., Lawas, L., Lebow, H., Lawas, A., Handerson, N., Mangum, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor, M., Mallor
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                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-MAY-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Rat Genome Sequencing Consortium.
***, 3 unordered pieces. AC120668
                                                              AC120668.4 GI:25188255
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                                                                                                                                                                                                                                                                 (bases 1 to 250169)
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Direct Submission
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                                                                                                                    SOURCE
ORGANISM
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                                   ACCESSION
                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                 REFERENCE
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On Nov 23, 2002 this sequence version replaced gi:23322270. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Sstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Phrap, version 0.990329
Consensus quality: 225414 bases at least Q40
Consensus quality: 228258 bases at least Q30
Consensus quality: 229994 bases at least Q20
Estimated insert size: 228717; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 9799: contig of 9799 bp in length 9800 9899: gap of unknown length 18558 249057: contig of 239058 bp in length 9958 250169: contig of 1112 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
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Center clone name: CH230-24K10
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clone_end:T7"
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clone_end:T7"
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9900. .10968
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245037. .246234
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/note="clone_boundary
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11406. .14106
/note="wgs_contig"
complement (234439. .
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                                                                                                                                                  If the Bac Library Name is LB1 to LB4, please see website for the description: http://www-geal.lb1.gov/chenglpAC.html These libraries are available through the BACPAC Resources Center: http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTIGGGCATGIACATTITIGGCAGCCIAGGCTGTGTACATGIGTACACATTCTGAACAT 737
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Danio rerio (zebrafish)
Danio rerio (zebrafish)
Bulio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Meopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             618 AGCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAAATCCAATAGAAAGTTAAATT
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Lagan (http://lagan.stanford.edu/) and paired end information.
                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrag version 0.990329.

* NOTE: This is a "working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 33276: contig of 33275 bp in length
* 33275: contig of 33275 bp in length
* 54252 54351: gap of unknown length
* 54352 557331: contig of 11382 bp in length
* 5534 127515: contig of the submit length
* 5534 127515: contig of the submit length
* 5534 127515: contig of the submit length
* 127516 127515: contig of the submit length
* 127516 127515: contig of the submit length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         have
                                                                                            Programs for Genomic Applications (NHLBI)
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8.8%; Score 68.6; DB 2;
Best Local Similarity 62.3%; Pred. No. 2.9e-05;
Matches 124; Conservative 0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Atelerix albiventris"
/mol type="genomic DNA"
/db_xref="taxon:9368"
/clone="LB4-81H3"
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                                                                                                                                                                                                                                                                                                                                                                                             191796 CCCTAGTGGTAAAACAAGAGAGAGTGAATCAAATACCTATCTGTCTTTTTATGCAACCAT 191737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191736 TCTGAGGAGAGTTTGGGTGCTGCATGATCCAACGATGAGTCATTTAGTGGTGTTGTGGTG 191677
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Direct Submission
Submitted (07-AUG-2003) Genome Sciences, Lawrence Berkeley National
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                                                                                                                                                                                                                                                                                                                                          485 TGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGA----TGTTTCTTTTATGAAATAAT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 ACTITIAGAGAATAGAAAGCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAATCC 660
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                                                                                                                                                                                                                 TATCGTCATTCATGTGACATAAAAG-----ATGGAAAGGGGCTTCATGTTAGTGA
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                                      Gaps
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Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, B.M.
Direct Submission
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Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
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On Aug 7, 2003 this sequence version replaced gi:29294044.
                                      10;
      Pred. No. 9.8e-10;
0; Mismatches 109; Indels
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HTG; HTGS PHASE2; HTGS DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
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   60.7%; Pred. No.
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Center Code: PGABERK
Center Project Name: B015
Bac Clone Name: LB4-8113
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Best Local Similarity 60.7
Matches 184; Conservative
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DNA linear HTG 11-OCT-2004
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Cyptiniformes, Cyptinidae, Danio.
(bases 1 to 145160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 11, 2004 this sequence version replaced gi:54019745.
     619 GCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAATCCAATAGAGAAGGTAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141804 bases at least Q40
Consensus quality: 142048 bases at least Q30
Consensus quality: 142175 bases at least Q20
Insert size: 14560; sum-of-contigs
Insert size: 150827; 3.5% error; agarose-fp
Quality coverage: 11.77x in Q20 bases; sum-of-contigs Quality
coverage: 11.28x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently tonsists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                               Danio rerio clone CH211-194N10, unordered pieces.
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HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159590 TTTTAAAACCTAAAAGTTTCTATAACTATTGTGTTTTTTGCCCTGATTACAGTACATCATAT 159649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 ATTAATCCTTTTAAGGTCTAGTTTTTCTTAAGTCTGTGCAGTAATAGAGGT--ATCGTCA 438
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                                                                        Direct Submission
Submitted (13-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 13, 2003 this sequence version replaced gi:32567584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived bebrafish pUC subclones occasionally display inconsistency over th length of mononuclecties or truns and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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48.5%; Pred. No. 0.081;
ive 0; Mismatches 185; Indels 2
                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Cypriniformes; Cyprinidae; Danio. (bases 1 to 183103)
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
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VECTOR: pindigoBAC-5
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                                               Barlow, K.
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Best Local
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10276 TIGIATATIGICAAAATIGICITITITI 10303
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1 tcatgtaggtaagactgtgt......gtctctttttattgttaag 777 US-09-463-542-34_COPY_368_1144 score: Sequence: Title: Perfect :

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	2000	moradi naga	Aax19034 Human PPA	Ads36461 Human aut	Aax19065 Human PPA	Ads39355 Human aut	Ads39165 Human aut		Ads39163 Human aut	Abn80072 Human che	Abl32312 Human imm	Abl54333 Chemicall	Abk39937 Human che	Abl32219 Human imm		Abl54364 Chemicall	Abk31322 Signal tr	Abl70293 Chemicall	Aas61223 Human gen	Aas46343 Tumour su	Abk31250 Signal tr	Abg67006 Human ang
SOMMERTES	Ę		AAX19034	ADS36461	AAX19065	ADS39355	ADS39165	ADS39169	ADS39163	ABN80072	ABL32312	ABL54333	ABK39937	ABL32219	ABK31423	ABL54364	ABK31322	ABL70293	AAS61223	AAS46343	ABK31250	ABQ67006
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	2		777	764.2	383	200.6	200.6	196.6	195.8	20	49.2	49.2	49	49	48.4	48.4	47	47	47	46.8	46.8	46.6
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ALIGNMENTS

Human PPAR-gamma-3 proximal promoter, exon A2 and intron A2. BP. AAX19034 standard; DNA; 1463 (first entry) 13-MAY-1999 AAX19034; AAX19034

Human, peroxisome proliferator activated receptor gamma; PPAR-gamma, regulatory sequence; promoter; obesity; anorexia; lipoma; cachexia; lipodystrophy, liposarcoma; human immunodeficiency virus; HIV; insulin resistance, non-insulin-dependent diabetes mellitus; polycystic ovary syndrome; gastrointestinal tract; Crohn's disease; inflammatory bowel disease; ulcerative colitis; bowel cancer; ss.

Homo sapiens

WO9905161-A1.

04-FEB-1999.

98WO-US015411. 24-JUL-1998;

97US-0053692P 25-JUL-1997;

PHARM INC. (LIGA-) LIGAND PHARM (INSP) INST PASTEUR ä Auwerx J, Fajas Saladin RS, Briggs MR,

WPI; 1999-142844/12.

Newly isolated nucleic acid comprising a control region of a human peroxisome proliferator activated receptor (PPRA) gamma gene - useful for identifying modulators that are useful in treating diseases associated with abnormal levels of human PPAR-gamma gene expression.

Claim 11; Page 88; 102pp; English.

The present invention describes an isolated, purified or enriched nucleic acid comprising a control region of a human peroxisome proliferator

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cc activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful for screening for agents capable of modulating the expression of a human PPAR-gamma gene. These agents (modulators) form pharmaceutical compositions that are useful for treating diseases associated with high/low levels of human PPAR-gamma gene expression. The diseases include Obesity, anorexia, cachexia, lipodystrophy, lipomas, liposarcomas, abnormalities associated with anti-human immunodeficiency virus (HIV) treatment, insulin resistance, non-insulin-dependent diabetes mellitus abnormalities associated with anti-human immunodeficiency virus (HIV) tract, inflammatory bowel disease, Crohn's diseases of the gastrointestinal (GI) tract, inflammatory bowel disease, crohn's disease, ulcerative colities and bowel cancer. The nucleic acids are useful for studying the role of the PPAR-gamma gene in various diseases and disorders. The structure of PPAR-gamma enables genetic studies of PPAR- gamma mutations in humans, and evaluation of its role in disorders like insulin resistance, NIDDW, and diseases associated with altered adipose tissue function, like obesity and the production of transgenic animals, which are useful in screening for modulators of the human PPAR-gamma gene syspension. The present sequence useful in designing drugs for treating disorders or diseases associated with the level of PPAR-gamma -3 proximal promoter, exon A2 and intron A2 crosses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1463 BP; 461 A; 228 C; 284 G; 490 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
1es 777; Conservative
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The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autorimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single of polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for diagnosing and treating autoimmune disease, such as: rheumatoid arthritis, type 1 dispetes, multiple sclerosis, systemic lupus erythematosus, inflammatory consemia, asthma, vitiligo, glomarionephritis, Grave's disease, pernicious anaemia, asthma, vitiligo, glomarionophritis, Grave's disease, mycarditis, Sjogren's disease, or primary systemic vasculitis. The present nucleic acid represents a human autoimmune disease-related genomic DNA sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the NIPO website.
                    1028 AATAGAGAAGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGT 1087
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AATAGAGAAGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGT 720
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                                                                                              Sequence 158417 BP; 47887 A; 30186 C; 31475 G; 48577 T; 0 U; 292 Other;
                                                                          1 TCATGTAGGTAAGACTGTGTAGAATGTCGGGTCTCGATGTTGGCGCTATTCAAGCCCTGA
                                                                                                                                                                                                                                                                                                                                                                 single nucleotide polymorphism detection; sheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephitis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
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; Pred. No. 1.3e-
4; Mismatches
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98.6%;
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25-APR-2003; 2003US-0465241P.
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Best Local Similarity 98.63
Matches 766; Conservative
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The present invention describes an isolated, purified or enriched nucleic acid comprising a control region of a human peroxisome proliferator acid comprising a control region of a human peroxisome proliferator activated receptor gamma (PPAR-gamma) gene. The nucleic acids are useful for screening for agents capable of modulating the expression of a human CC compositions that are useful for treating diseases associated with high/low levels of human PPAR-gamma gene expression. The diseases include obseity, anorexia, cachexia, lipodystrophy, lipomas, lipodascomas, cobsity, anorexia, cachexia, lipodystrophy, lipomas, lipodascomas, cobsity, anorexia, cachexia, lipodystrophy, lipomas, lipodascomas, cobsity, anorexia, cachexia, lipodystrophy, lipomas, lipodascomas, lipodascomas, lipodascomas, lipodascomas, lipodascomas, libodascomas, lipodascomas, lipodystrophic syndromes. The nucleic acids are also useful content diseases associated with altered adipose tissue function, like consenting assays. The control regions of the nucleic acids are elso cuseful in screening sassays. The control regions of the nucleic acids are useful cuseful in designing drugs for treating disorders or diseases associated with altered adipose tissue secondar acids cuseful in designing drugs for treating disorders or diseases associated with altered adipose tissue secondar acids cuseful in designing drugs for treating disorders or diseases associated with altered adipose tissue secondar acids cuseful in designing drugs for treating disorders or diseases associated with altered adipose tissue secondar acids cuseful in designing drugs for treating disorders or diseases associated with altered secondar secondar secondar secondar secondar secondar secondar secondar secondar secondar secondar secondar secondared secondar secondar secondar secondar secondar secondar seconda
                                                                                                                                                                                                                                                     Newly isolated nucleic acid comprising a control region of a human peroxisome proliferator activated receptor (PPAR) gamma gene - useful identifying modulators that are useful in treating diseases associated with abnormal levels of human PPAR-gamma gene expression.
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                                                       TGATAAGGCTTTTGGCATTAGATGCTGTTTTGTCTTCATGGAAAATACAGCTATTCTAGG
                                                                           ATCCTTGAGCCTTTCATAAGAGATAAGGTTGTGAATCCTAAGACCCTAGGACCATTTACT
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The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SMP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for disgnosing and treating autoimmune disease, such as rheumatoid arthritis, type I dispetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia, asthma, vitiligo, glomerilonephitis, Grave's disease, pernicious myocarditis, sjogren's disease, or primary systemic vasculitis. The present DNA sequence represents a human autoimmune disease. Tealated genomic-based SNP context sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from
300 GGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGTGTACACATTCTGAACATGTGTG 359
                                                                                                                                                                                                                                                                                                                                                 single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythemateorus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; permicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
                                                                                                                                                                                                                                                                                                            Human autoimmune disease-related SNP context sequence - SEQ ID 4569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
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                                      TATATTGAAAATCTTGTCTCTTTTTTTTTTAAG
                                                                             360 rararrgaaarcrrcrcrrrrrrarrgrraag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; SEQ ID NO 4569; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             primary systemic vasculitis; ds.
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25-APR-2003; 2003US-0465241P.
                                                                                                                                                                                   ADS39355 standard; DNA; 201
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The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autorimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA creating autoimmune disease, acomprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA treating autoimmune disease, servine useful for disquesting and treating autoimmune disease, servine, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory comportations and and and an acid disease, peoritais, thyroiditis, celiac disease, pennicious and ania, asthma, vitiligo, glomerulonephritis, drave's disease, myocarditis, Sjogren's disease, or primary systemic vasculitis. The present present DNA sequence represents a human autoimmune disease-related genomic-based SNP context sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the WIPPO website.
                                       120
                                                                                                   281
                                       61 GACCCTAGGACCATTTACTTAGATGATCTCTCTCTCTCGTTYGTCCTCTGAAAAGTCTGCT
                                                                              TCGTGAGGGGTGTGCTGCTTTGCCTTGCCTAAGTGGTGTGGGCACACAACTGTACTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         single nucleotide polymorphism detection; sNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human autoimmune disease-related SNP context sequence - SEQ ID 4379
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162 GACCCTAGGACCATTTACTTAGATGATCTGCTCTCTGGTTCGTCCT
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25-APR-2003; 2003US-0465241P.
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25.8%; Score 200.6; DB 13; Length 201; 99.5%; Pred. No. 4.4e-40; ive 1; Mismatches 0; Indels 0;

Best Local Similarity 99.5 Matches 200; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SMP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for disquosing and treating autoimmune diseases, such as: rheumatoid arthritis, type I diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory
                                                                       184
                                                                                                                                                                     304
                                                                                                                      244
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                                                                                                                                                                                         CCTTGCCTAAGTGGTGTGGCACACAACTGTACTGTCACCTTAGGCTTAATAACCATGTGT
                                                                       TTGAGCCTTTCATAAGAGATAAGGTTGTGAATCCTAAGACCCTAGGACCATTTACTTAGA
                                                                                              Transcrittchinadagaranaggrigiganiccinagacccinagaccaritinctinga
                                                                                                                       TGATCTGCTCTCTGGTTCGTCCTCTGAAAAGTCTGCTTCGTGAGGGGTGTGCTGCATTTG
                                                                                                                                    TGATCTGCTCTCTGGTTCGTCCTCTGAAAAGTCTGCTTCGYGAGGGGTGTGCTGCTTTG
                                                                                                                                                                     CCTTGCCTAAGTGGTGTGGCACACACTGTACTGTCACCTTAGGCTTAATAACCATGTGT
                                                                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                Human autoimmune disease-related SNP context sequence - SEQ ID 4383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
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                         DB 13; Length 201;
                                                0; Indels
Seguence 201 BP; 48 A; 41 C; 46 G; 65 T; 0 U; 1 Other;
                      Score 200.6; DB 1
Pred. No. 4.4e-40;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; SEQ ID NO 4383; 123pp; English.
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                                                                                                                                                                                                                      CATCTAGAATGAAGTTATATT 325
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                        25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2003; 2003US-0465241P
                                                                                                                                                                                                                                                                                                          ADS39169 standard; DNA; 201
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                               Matches 200; Conservative
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                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                         16-DEC-2004
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                        Query Match
Best Local
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bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious anaemia, aethma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sigoren's disease, or primary systemic vasculitis. The present DNA sequence represents a human autoimmune disease-related seguence. La present sequence of the invention. NoTE: The present sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TCATGTAGGTAAGACTGTGTAGAATGTCGGGTCTCGATGTTGGGGGCTATTCAAGCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATAAGGCTTTTGGCATTAGATGCTGTTTTGTCTTCATGGAAAATACAGCTATTCTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCATGTAGGTAAGACTGTGTAGAATGTCGGGTCTCGATGTTGGCGCTATTCAAGCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephitis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
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                                                                                                                                                                                                                                                                                                    Score 196.6; DB 13; Length 201;
Pred. No. 4.3e-39;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                Sequence 201 BP; 50 A; 35 C; 47 G; 68 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; SEQ ID NO 4377; 123pp; English.
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99.5%;
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25-APR-2003; 2003US-0465241P.
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                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.5
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (APPL-) APPLERA CORP.
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                                                                                                                                                                                                                                                                                                          Query Match
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genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for disgnosing and treating autoimmune diseases, such as: rheumatoid arthritis, type I diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel diseases, psoriasis, thyroiditis, caliac disease, pernicious anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sjogren's disease, or primary systemic vasculitis. The present DNA sequence represents a human autoimmune disease-related genomic-based SNP context sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the WIPO website.
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Sequence 201 BP; 62 A; 22 C; 46 G; 70 T; 0 U; 1 Other;

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                                                                   411 AGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGGTGGAAAGGGGGCTTC 470
                                                                                                                           471 ATTCATGTTAGTGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGATGTTTCTTTT 530
                                                                                                                                            61 ATTCATGTTAGTGGAAGTAGGAAAGTAGGTGAAGTGAWTCTAATAGATGTTTCTTTT 120
                                                                                                                                                                                    ATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTGTGG 590
                                                                                                                                                                                                    ATGAAATAATTTTTAAAAGATTCTCCCAGCCCTGCATGATTTATGATGATGATTTTGTGG 180
                                                                                    Gaps
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           DB 13; Length 201;
Score 195.8; DB 13; Louis
Pred. No. 6.8e-39;
Pred. Tritches 3; Indels
                                      1, Mismatches
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                                                                                                                                                                                                                                                              25.2%; (98.0%;
                                     Matches 197; Conservative
                       Best Local Similarity
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          Query Match
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Human chemically modified disease associated gene SEQ ID NO 89. ABN80072 standard; DNA; 5771 BP (first entry) 15-JUL-2002 ABN80072 RESULT 8

Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone descetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.

sapiens Synthetic Ношо

WO200200927-A2.

03-JAN-2002

30-JUN-2000; 2000DE-01032529. 01-SEP-2000; 2000DE-01043826.

02-JUL-2001; 2001WO-EP007536

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2002-130908/17.

Novel nucleic acid useful for diagnosis and therapy of diseases

Homo sapiens

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is sequences (ABN79984-ABN80333) or their complements. The invention is development genes, in particular disease associated with companital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related to histone deacetylation, Currarino syndrome, diseases related with the chypanent of the brain and limb girdle muscular dystrophy and dwarfism. Colliquers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and or this spatent did not form part of the printed specification but is based on patent did not form part of the printed specification but is based on patent did not form part of the printed specification but is based on 1578 ö 428 489 AATAGGAAAGTAGGTGAAGTGATTTTAATAGATGTTTCTTTTATGAAATAATTTTTAAAA 548 associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development. antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulaant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye dlaease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; sequence information supplied to Derwent by the European Patent Office 309 TAGAATGAAGTTATATTTTAAAAAGGATCGTTTTTGCCATGTATAAATTTTTCAAACATTA 369 ACTITCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTTTTAAGTCTGTGCAGTAATAGA 1519 TTATTTTTGTATAGTATTTTTTTTTTTGGTTAATTTTTATTTTATGTTAAAGTTGTAGT Gaps system disease; cytosine methylation; antiasthmatic; ö Sequence 5771 BP; 1877 A; 37 C; 980 G; 2877 T; 0 U; 0 Other; Length 5771; Score 50; DB 6; Length 577 Pred. No. 0.033; 0; Mismatches 155; Indels Human immune system associated gene SEQ ID NO: 285. English BP. ABL32312 standard; DNA; 18683 Claim 1; SEQ ID NO 89; 27pp; 6.4%; (first entry) Query Match Best Local Similarity 48.0° Matches 143; Conservative 26-MAR-2002 ABL32312; ABL32312 RESULT 셤 g g ò g 셤 ઠે ઠે δ ઠે

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                                                                                                                                                                                                                                                                                                                                                                        system associated
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                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, ancer, acute myeloid leukeemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18683 BP; 5439 A; 130 C; 3594 G; 9520 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3%; Score 49.2; DB 6; Length 18683; Best Local Similarity 46.5%; Pred. No. 0.072; Matches 228; Conservative 0; Mismatches 258; Indels 4;
                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 285; 32pp + Sequence Listing; German
                                                                  02-JUL-2001; 2001WO-EP007537.
                                                                                                   30-JUN-2000; 2000DE-01032529.
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                                                                                                                                                      (EPIG-) BPIGENOMICS AG
                                                                                                                                                                                                                          WPI; 2002-130909/17.
WO200200928-A2
                                                                                                                                                                                                                                                                                                  methylation.
                                 03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis, HIV, Bloom syndrome, cardiopathy; neurodegenerative disorder; Herpes simplex virus; renal ischaemia, amyotrophic lateral sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
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Pred. No. 0.072;
0; Mismatches 258;
                                                                                                                                                                                                                       Chemically treated apoptosis gene #17
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                                 BP.
                                 ABL54333 standard; DNA; 18683
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07-APR-2000; 2000DB-01019173.
30-JUN-2000; 2000DB-01035529.
01-SBP-2000; 2000DB-01043828.
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Matches 228; Conservative
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ABL54333
ID ABL
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes ascordated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 000593), CYP11A (NM 000731), CYP1B1 (NM 000497), CYP3A3 (NM 000776 and NM 017460), DPYD (NM 000310), CYP1B1 (NM 001979), OCLN (NM 000776 and NM 019901, NM 019902, NM 019902, NM 019903, NM 019903, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019962, NM 019909, NM 019901, NM 019902, NM 019902, NM 019902, NM 019909, NM 019909, NM 019901, NM 019902, NM 019902, NM 019909, NM 019901, NM 019902, NM 019902, NM 019909, NM 019901, NM 019902, NM 019902, NM 019909, NM 019901, NM 019902, NM 019902, NM 019909, NM 019901, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902
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TTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTG
                                                                                                      TGGTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGCTCAGGGAAAGC--AAACA
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cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXI
UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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01-SEP-2000;
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analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers. The 84 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarthritic; antidiabetic; antipsoriatic; antiantilnilammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimear's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                            570 TTATGATGAATCATTTTGTGGTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGC
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                                                                                                                                                                                                                                        7;
                                                                                                                                                                       Sequence 11422 BP; 3913 A; 59 C; 1856 G; 5594 T; 0 U; 0 Other;
                                                                                                                                                                                                         Length 11422;
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                                                                                                                                                                                                       DB 6;
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Pred. No. 0.071;
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                 1034 AATTTTATAAAAGAGATATATTTGTTAATTTGTAGTGTATATGTTTTGGAGAATATATTT 7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argiririraagarriraagacgiajararririraaagirgirarra----ri 6733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6854 TTGAATGGATGTTTTTGATATGTATTTTTTTTAATTTTTATATTTTAATATTTATTTAA 6913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid retweemia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                           272 TGTACTGTCACCTTAGGCTTAATAACCATGTGTCATCTAGAATGAAGTTATATTTTAAAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AGGATCGTTTTTGCCATGTATAAATTTTCAAACATTAACTTTCAGGGTTATTAATCCTTT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 AAAGATGGAAAGGGGCTTCATTCATGTTAGTGAAATAGGAAAGTAGGTGAAGTGAT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITAATAGAIGITICTITIAIGAAATAATITITIAA--AAGAITGICCAGCCCTGCAIGAT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATGATGAATCATTTTGTGCTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGC 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 TACATTTTGGCAGCCTAGGCTGTGTACATGTGTACACATTCTGAACATGTGTGTATATTG 749
                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                           Sequence 11422 BP; 3913 A; 59 C; 1856 G; 5594 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                6.3%; Score 49; DB 6; Length 11422;
16.4%; Pred. No. 0.071;
ive 0; Mismatches 265; Indels '
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 192; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7094 ATCTTTTGGCGTTTATTTTTTTGAA 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 AAAATCTTGTCTCTTTTTTTTTTAT 776
                                                                                                                                Berlin K;
                                                                         30-JUN-2000; 2000DE-01032529.
                                                    02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.4%;
Matches 235; Conservative
                                                                                                                                Dlek A, Piepenbrock C,
                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                     WPI; 2002-130909/17
         WO200200928-A2.
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                                03-JAN-2002
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disclosed are oligomuclectides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell innes, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2533 TTTTGTTTTAATTATTTATGTATTTTTTTAGTTTTGATAGCGTTTAGTTTTATTGATTTT 2592
                                                                                                                                                                                                                                                                                                          Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease, solid tumour, cancer, antitumour, cytostatic, mutant, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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                                                                                                                                                                                                                                 Signal transduction associated gene modified complementary DNA #133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 13123;
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19.1%; Pred. No. 0.1;
ve 0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 266; 24pp; English
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    ВЪ.
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ABK31423 standard; DNA; 13123
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 49.19
Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                            ABK31423
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TTAGGCTTAATAACCATGTGTCATCTAGAATGAAGTTATATATTTTAAAAAGGATCGTTTTT

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2593 rititinitigaragartiaaiargögiairaartritiriaiaagritairtai 2652
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                                                                                                                                                                                                                                                                                            GTTTCTTTTATGAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATC 581
TITITICITAAGICIGIGCAGIAATAGAGGIATCGICAITCAIGIGACAIAAAAGAIGGAA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis; HIV; Bloom syndrome; cardiopathy; neurodegenerative disorder; Herpes simplex virus; renal ischaemia; amyotrophic lateral sclerosis;
                                                                                                                                                  462 AGGGGCTTCATTCATGTTAGTGATGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemically treated apoptosis gene complementary to gene #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Seq ID #64; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               601
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                                                                                                                                                                                                                                                                                                                                                                                                                                               582 ATTITGIGGICTGITAGITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL54364 standard; DNA; 13123
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07-APR-2000; 2000DB-01019173.
30-JUN-2000; 2000DB-01032529.
01-SEP-2000; 2000DB-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease, solid tumour, cancer, antitumour, cytostatic, mutant, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cellines, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
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                                             344 GCCATGTATAAATTTTCAAACATTAACTT--TCAGGGTTATTAATCCTTTTAAGGTCTAG
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                                                                                                                 TITITCTTAAGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGATGGAA
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01-SEP-2000; 2000DE-01043826
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brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
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Sequence 6880 BP; 2032 A; 49 C; 1380 G; 3419 T; 0 U; 0 Other;

478 301 GIGICATCIAGAAIGAAGTIATATTITIAAA--AGGATCGITITITGCCATGIATAAATIT 358 TCAAACATTAACTTTCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTCTTAAGTCTGTG 418 rgraceritrratiriterratiritritritriterritritritritritritritritaeadecratra 841 901 TAGTGATGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGATGTTTCTTTTATGAAATA 538 961 TITIAATATITAAATITITAGTAGTITITAGGGGTATAAGTGGTITITIGATTATATGGATGA 2; Gaps Score 47; DB 6; Length 6880; Pred. No. 0.19; 0; Mismatches 120; Indels Query Match 6.0%; Best Local Similarity 51.8%; Matches 131; Conservative ATTITIAAAAGAT 551 ATTGTATAGAAAT 974 359 782 479 902 539 962 ሯ 셤 ò g ò 셤 ò 원 ò

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APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

FRIOR PILING DATE: 1998-02-13

PRIOR PELICATION NUMBER: US 60/074,725

PRIOR PELING DATE: 1998-02-13

PRIOR PELING DATE: 1998-02-13

FRIOR PELING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

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US-09-949-016-56719
US-08-11-210A-80
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US-08-11-218-16
US-08-11-809-3
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US-09-949-016-15954
; Sequence 15954, Application US/09949016
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Best Local Similarity
Matches 124; Conserv
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             SERVETAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SETOR PILING DATE: 2000-10-03

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15954

LENGTH: 54576
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Patent No. 6812339

GENERAL INFORMATION:
FORTHER, USENTER, J. Craig et al.
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF ILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR RILING DATE: 2000-10-03
FRIOR RILING DATE: 2000-10-03
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Pred. No. 0.16;
0; Mismatches 136; Indels
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LOCATION: (1)...(54576)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 50.0%;
Matches 137; Conservative
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APPLICATE: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16110

LENGTH: 231129
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                                                                                                                                                         Score 44.4; DB 4; Length 54576; Pred. No. 0.16; 0; Mismatches 136; Indels 1;
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45.5%; Pred. No. 1.3;
iive 0; Mismatches 177;
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Patent No. 6812339
GENERAL INFORMATION:
                                             i LOCATION: (1)...(54576)

j OTHER INFORMATION: n = A,T,C or
US-09-949-016-15955
                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 137; Conservative
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Best Local Similarity 45.5
Matches 148; Conservative
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Human
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Patent No. 6812339
GENERAL INFORMATION:
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                                                               525 TCTTTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATT
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                                                                                                                                                                                                                                                                                                                                      72876 ATATATTATATATATATATA 72900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60040 ATATATTATATATATATATA 60064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          585 TTGTGGTCTGTTAGTTACTTTTAGA 609
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US-09-949-016-156335/c
; Sequence 156535, Application US/09949016
; Patent No. 6812339
; GENERAL INPORMATION:
; APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-949-016-11934
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LENGTH: 266293
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLOOL307
CURRENT PILLOR EFFERENCE: CLOOL307
CURRENT PILLOR DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILLING DATE: 2000-10-20
PRIOR PILLING DATE: 2000-10-20
PRIOR PILLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-01-0-03
PRIOR FILING DATE: 2000-01-0-03
PRIOR FILING DATE: 2000-01-0-03
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 GGCTTCATTTTTATTAGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGATGTT
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Sequence 22, Application US/09806708B

Sequence 22, Application US/09806708B

Sequence 22, Application US/09806708B

SERENT NO. 6784342

TOTAL OF INVENTION: Regulation of Embryonic Transcription in Plants

TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03

PRIOR PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 23

NUMBER OF SEQ ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.4; DB 4; Length 601;
Pred. No. 0.23;
1; Mismatches 177; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial sequence
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; ORGANISM: Human
US-09-949-016-156535
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Sequence 13173, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION WITHER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREEESE FREEESEQ for Windows Version 4.0

SEQ ID NO 13173

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                                                               316 AAGTTATATTTTAAAAAGGATCGTTTTTGCCATGTATAAATTTTCAAACATTAACTTTCA 375
                                                                                         695 WWNNTDARRINNTTVWRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNNNNNNNNSCC 636
                                                                                                                                                                          635 TCTRAMIMRATMKGDGMIVRKKVKWKWRDITCTYVDVWADSWVWWYANWMRCRDVTYTRNNT 576
                                                                                                                                              376 GGGTTATTAATCCTTTTAAGGTCTAGTTTTTCTTAAGTCTGTGCAGTAATAGAGGTATCG 435
                                                                                                                                                                                                                             496 AAGTAGGTGAAGTGATTTTAATAGATGTTTCTTTTATGAAATATTTTTAAAAGATTGTC 555
                                                                                                                                                                                                                                                                                                                                     616 AAAGCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAATCCAATAGAGAAGGTAAA 675
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46.5%; Pred. No. 3.5;
tive 0; Mismatches 151; Indels 0;
Best Local Similarity 9.3%; Pred. No. 0.52;
Matches 34; Conservative 155; Mismatches 178; Indels
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Best Local Simil
Matches 131, C
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GENERAL INCORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR PELING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESECTED WINDOWS Version 4.0
SEQ ID NO 14353
LENGTH: 175236
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Batent No. 6812339
GENERAL INFORMATION:
TATLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REPREBACE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 2000-09-08
NUMBER OF SEQ 1D NOS: 207012
                                                           107752 AGCTCTTGTCTGATATTACTGCTGCAGGCTTTATTTTGATTAGCATTTTCCTAGTATGTA 107811
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472 TTCATGTTAGTGATGGAAATAGGAAAGTAGGTGAGTGATTTTAATAGATGTTTTTA
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48.1%; Pred. No. 4;
tive 0; Mismatches 122; Indels
                                                                                                                             TGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTAT
                                                                                                                                                                                                                                                                                                                                                         Sequence 14353, Application US/09949016 Patent No. 6812339
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Best Local Similarity 48.13
Matches 113; Conservative
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US-09-949-016-16600/c
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Sequence 142482, Application US/09949016

Sequence 142482, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FasteEQ for Windows Version 4.0
         505 AAGTGATTTTAATAGATGTTTCTTTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGC 564
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                                                                                          TITAAAAAGGATCGTTTTTGCCATGTATAAATTTTCAAACATTAACTTTCAGGGTTATTA
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46.5%; Pred. No. 1;
ive 0; Mismatches 145; Indels
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Best Local Similarity 46.5
Matches 126; Conservative
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US-09-949-016-142482/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; CURRENT APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                 528 TTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTG
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1)...(298336)
OTHER INFORMATION: n = A,T,C or
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                        SEQ ID NO 16600
LENGTH: 298336
TYPE: DNA
ORGANISM: Human
PEATURE:
                                                                                                                                                                                                                                                            US-09-949-016-16600
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US-09-806-708B-22
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LOCATION: 96..167
NAME/KEY: 3'UTR
LOCATION: 168..1783
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LENGTH: 1783
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/291,755
PRIOR APPLICATION NUMBER: 60/291,756
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-010-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12372
LENGTH: 181429
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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                                       286 İTTGGACTAAGTACCAAAATGACCACATTTTTGİGAAĞTGGCCAAGTAAAĞTTTTAA 227
                                                                                                                    325 TTTAAAAAGGATCGTTTTTGCCATGTATAAATTTTCAAACATTAACTTTCAGGGTTATTA 384
445 IGACATAAAAGATGGAAAGGGGCTTCATTCATGTTAGTGAAGTAGGAAAGTAGGTA
                                                                                        505 AAGTGATTTTAATAGATGTTTCTTTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGC 564
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Best Local Similarity 46.5%; Pred. No. 6.6;
Matches 126; Conservative 0; Mismatches 145; Indels
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JOURNALL INFORMATION:
JAPPLICANT: Cohen, Daniel
JAPPLICANT: Chen, Daniel
JAPPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
JAPPLICANT: Bouqueleret, Lydie
JAPPLICANT: Bealoux, Laurent
TITUE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENE, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: 53.US15.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT APPLICATION NUMBER: 09/39,333
PRIOR APPLICATION NUMBER: 09/39,333
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR APPLICATION NUMBER: 60/168,088
PRIOR FILING DATE: 1999-11-30
NUMBER: OF SEQ ID NOS: 134
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0; Mismatches 145; Indels
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CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 6/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 6/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 6/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1572
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46.5%; Pred. No.
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Patent No. 6555316
GENERAL INFORMATION:
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Best Local Similarity
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LOCATION: 1..95
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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1237 caaaattattettaerttagatrttagaagaattaagtaaaagaateageeaggagtic 1178
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4.9%; Score 38.4; DB 4; Length 1783;
Best Local Similarity 45.9%; Pred. No. 2.1;
Matches 168; Conservative 0; Mismatches 196; Indels 2; Gaps
; NAME/KEY: polyA signal
; LOCATION: 1757._1762
; NAME/KEY: allele
; LOCATION: 132
; OTHER INFORMATION: 8-130-143 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 132
; OTHER INFORMATION: 8-126-286 : polymorphic base A or G
US-09-679-409-9
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Sequence 285, App
Sequence 33, Appl
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Sequence 18, Appl
Sequence 64, Appl
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-311-455-192
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US-10-311-455-285

i Sequence 285, Application US/10311455

i Sequence 285, Application US/10311455

i CENERAL INFORMATION:

APPLICANT: DLEK, Alexander

APPLICANT: DLEK, Alexander

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT FILING DATE: 2002-12-16

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-37

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 2424

SEG ID NOS: 2424
                                                                                   Sequence 256988,
Sequence 2, Appli
Sequence 183, App
Sequence 65, Appl
Sequence 36, Appli
Sequence 1, Appli
                                                                                                                                                                                                    Sequence 26, Applesquence 25, Applesquence 5299, Applesquence 1346, Applesquence 186, Applesquence 2186, Applesquence 167, Applesquence 1675, Applesquence 1675, Applesquence 776150, Sequence 776150,
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1118, Ap
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13 US-09-925-065A-814225

14 US-10-027-632-256987

18 US-10-027-632-256988

18 US-10-027-632-256988

18 US-10-027-632-256988

18 US-10-027-632-256988

19 US-10-312-841-2

20 US-10-317-44A-65

20 US-10-317-441-16

21 US-10-311-455-1346

22 US-10-311-455-1346

23 US-09-398-842A-5299

24 US-09-398-842A-5299

25 US-10-311-455-1346

26 US-10-311-455-1346

27 US-10-311-455-1349

28 US-10-311-455-1389

29 US-09-925-065A-776150

20 US-10-311-455-1389

20 US-09-925-065A-790118

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22 US-10-311-455-1389

23 US-09-925-065A-790118

24 US-10-211-613-381

25 US-01-311-455-389

26 US-10-211-414-1188

27 US-02-318-842A-3892

28 US-10-21-613-347

29 US-02-311-455-339

20 US-02-311-455-339

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24 US-10-221-714A-144

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ORGANISM: Artificial Sequence
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1693 1
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6880 1
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Publication No. US20030162194A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis
FILE REPERENCE: 5013.1006
CURRENT PILING DATE: 2002-10-02
CURRENT PILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PRILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PRILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 78
SECOLD NOS: 78
                                                                                                                                                              350 TATAAATTTTCA--AACATTAACTTTCAGGGTTAATTAATCCTTTTAAGGTCTAGTTTTTC
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  Score 49.2; DB 16; Length 18683;
Pred. No. 0.45;
0; Mismatches 258; Indels 4;
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Query Match
Best Local Similarity 46.5%;
Matches 228; Conservative
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DB 17; Length 18683;

Score 49.2;

6.3%;

Query Match

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APPLICANT: DIEKENILOW:
APPLICANT: DIEKENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1922
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                                                                                                TATAAATITICA - - AACAITAACITICAGGGITATIAATCCITITAAGGICTAGITITIC
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                                                            TTAATAACCATGTGTCATCTAGAATGAAGTTATATTTTAAAAAGGATCGTTTTTGCCATG
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                    Gaps
                    4;
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Pred. No. 0.41;
0; Mismatches 265; Indele
  Pred. No. 0.45;
0; Mismatches 258; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 192, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.4%;
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
Best Local Similarity 46.5%;
Matches 228; Conservative
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1 Sequence 64, Application US/10240452

2 Publication No. US20030162194A1

3 FUBLICATION:

APPLICANT: OLEK, Alexander

3 APPLICANT: OLEK, Alexander

3 APPLICANT: OLEK, Alexander

3 APPLICANT: OLEK, Alexander

3 TITLE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis

3 TITLE OF INVENTION: Diagnosis of Diseases Associated with Apoptosis

3 TITLE OF INVENTION: DIAGNOSIS of Diseases Associated with Apoptosis

4 TILLE OF INVENTION: DIAGNOSIS of Diseases Associated with Apoptosis

5 TILLE OF INVENTION: UNMBER: US/10/240,452

5 CURRENT FILING DATE: 2002-10-02

5 FRIOR PELLING DATE: 2001-04-06

5 FRIOR APPLICATION NUMBER: DE 10019058.8

6 FRIOR APPLICATION NUMBER: DE 10019173.8

6 FRIOR PILING DATE: 2000-04-07

7 FRIOR PILING DATE: 2000-04-07

8 FRIOR FILING DATE: 2000-04-07

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-06-30

9 FRIOR FILING DATE: 2000-09-01

9 FRIOR FILING DATE: 2000-09-01

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1 FRIOR FILING DATE: 2000-09-01

1 FRIOR FILING DATE: 2000-09-01

1 FRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                 452 AAAGATGGAAAGGGGCTTCATTTCATGTTAGTGGAAATAGGAAAGTAGGTGAAGTGAT
                                                                                                                                                                                                                                                                                          512 TTTAATAGATGTTTCTTTTATGAAATAATTTTTAA--AAGATTGTCCAGCCCTGCATGAT
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                                                                                                        284 TTAGGCTTAATAACCATGTGATCTAGAATGAAGTTATATTTTAAAAAGGATCGTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13123;
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Best Local Similarity 49.1%;
Matches 157; Conservative 0
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ORGANISM: Artificial Sequence
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Publication No. US20040023230A1
GENERAL INFORMATION:
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APPLICANT: OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICAN OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO OLICANO O
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                                                                                                                                                                                                                              392 TAAGGICTAGTITITICTIAAGICTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITAATAGATGTTTCTTTTATGAAATAATTTTTAA--AAGATTGTCCAGCCCTGCATGAT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570 TTATGATGAATCATTTTGTGGTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGC 629
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                                                                                                                                                                                                                                                                                                                                                          AAAGATGGAAAGGGGCTTCATTCATGTTAGTGAAATAGGAAAGTAGGTGAAGTGAT
                                                                                                    AGGATCGTTTTTGCCATGTATAATTTTCAAACATTAACTTTCAGGGTTATTAATCCTTT
                                                                                                                                                                 5679 ATGTTTGTTTTAAGATTTAAAGACGTATATTATTTTTAAAGTAGTGTTTATTA----TT
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ORGANISM: Artificial Sequence
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2000-06-30
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SEQ ID NO 18
LENGTH: 11422
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212 TCTGAAAATGTATAAAGGATGGATATTAGACTCCCATGTTACATGTTACTTATTTTCGTGT 153
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Best Local Similarity 46.2<sup>3</sup>
Matches 159; Conservative
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                                                                                                                                  462 AGGGGCTTCATTCATGTTAGTGGAAATAGGAAAGTAGGTGAAGTGATTTTAATAGAT 521
                                                                                                                                                                                                                                                     GTTTCTTTTATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATC 581
                                                                                              411 AGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGATGGAAAGGGGGCTTC 470
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                  344 GCCATGTATAAATTTTCAAACATTAACTT--TCAGGGTTATTAATCCTTTTAAGGTCTAG
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PELING DATE: 2000-11-16
PRIOR PELING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PRECED for Windows Version 4.0
IENGTH: 595
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46.2%; Pred. No. 0.2;
iive 0; Mismatches 185; Indels
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Publication No. US20050228172A9
GENERAL INFORMATION:
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US-09-925-065A-814225
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Best Local S
Matches 159
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411 AGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGATGGAAAGGGGGCTTC 470
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                                                                                                                                                                                                                                                                             US-10-027-62-22-931/C

Sequence 256997, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

FRIOR PRIOR APPLICATION NUMBER: US 60/218,006

FRIOR PRIOR APPLICATION NUMBER: US 60/198,676

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 1999-11-23

FRIOR PELING DATE: 1999-01-23

FRIOR APPLICATION NUMBER: US 60/156,358

FRIOR PELING DATE: 1999-09-11-33

FRIOR PELING DATE: 1999-09-08

FRIOR FILING DATE: 1999-09-08

FRIOR FILING DATE: 1999-09-08

FRIOR FILING DATE: 1999-08-08

FRIOR FILING DATE: 1999-08-08

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46.2%; Pred. No. 0.31;
tive 0; Mismatches 185; Indels
711 GIGIACAIGIGIACACAIICIGAACAIGIGIGIAIAIIGAAAAI
                                                                                  152 TAATATAAAGAAGTAAATCTTAAGCATGTATGAATATTGAGAGT
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER: OF SEQ ID NOS: 325720
SEQ ID NO 256987
APPLICATION NUMBER: US 60/193,483
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: 108/10/027,632
CURRENT FILING DATE: 2000-204-30
PRIOR PILING DATE: 2000-07-12
PRIOR PLILOM DATE: US 60/198,676
PRIOR FILING DATE: US 60/198,676
PRIOR FILING DATE: US 60/198,676
              APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome
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0.31;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PELING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 1000-02-24
PRIOR PLING DATE: 1000-02-24
PRIOR PLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-09
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Pred. No.
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Best Local Similarity 46.2
Matches 159; Conservative
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US-10-027-632-256987/c
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US-10-027-632-256988
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475 AGCAGGIGGAAATITGAGGAAGIGIGTIGCAATCTACAGIGAACAIGGACTATTTCTAG 416
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APPLICANT: Wanstlow:
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE OF INVENTION: Dolymorphisms in the Human Genome
FILE OF INVENTION: Dolymorphisms in the Human Genome
FILE OF INVENTION: Dolymorphisms in the Human Genome
FILE OF INVENTION: DOLYMORER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/0218,006
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-03-29
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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PRIOR PILING DATE: 1999-08-28
PRIOR PILING DATE: 1999-08-28
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PRIOR PILING DATE: 1999-08-08
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                                                                                                         DB 18; Length 1693;
                                                                                                     Score 48; DB 18; Length 16:
Pred. No. 0.31;
0; Mismatches 185; Indels
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                                                                                                         6.2%;
                                                                                                     Query Match
Best Local Similarity 46.2<sup>3</sup>
Matches 159; Conservative
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ORGANISM: Human
US-10-027-632-256987
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TTATGATAATGAGAGTTTTGTTTTTTGTTTGTTTGTTTTTGTTTTGATTATAAGTATT 718060
                     GGTGAAGTGATTTTAATAGATGTTTCTTTTATGAAATAATTTTTAAAAGATTGTCCAGCC 560
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                                                            TCAAACATTAACTTTCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTTTAAGTCTGTG
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CURRENT APPLICATION NUMBER: US/10/221,613
PRIOR APPLICATION NUMBER: PCT/EP01/02945
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Best Local Similarity 51.8%; Pred. No. 1;
Matches 131; Conservative 0; Mismatches 120; Indels
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Publication No. US20040029123A1
GENERAL INFORMATION:
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DE 10019058 8
DE 1001917.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-03-15
2000-04-06
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ORGANISM: Artificial Seguence
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NUMBER OF SEQ ID NOS:
SEQ ID NO 183
LENGTH: 6880
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Publication No. US20030186277A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des IFIE REPERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                           411 AGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGATGGAAAGGGGGCTTC 470
                                                                                                                                                                                                                                                                    475 AGCAGGTGGAAAATTTGAGGAAGTGTGTTTGCAATCTACAGTGAACATGGACTATTTCTAG 416
                                                                                                                                                                                                                                                                                                                                                    AGCGAAGAAGTATTGGGATAAATGTTAGTGAGTGGTAAAGTGAGCACAGAGTTCTATT 356
                                                                                                                                                                                                                                                                                                                                                                                             531 ATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTGTGG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGCTCAGGGAAAGCAAACATTCAG 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGAAAGTGAAAAGTTAAACTGGGAGTCATAGTCTAAATATCTATTTAATATTTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 AATGAAATCCAATAGAGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTAAGTAATTTTTGCAAGACTTATCAGGGCAAAATGTCAGATTGCAATGGGTATTCTGA 296
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                                                                                                                                              DB 18; Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TAATATAAAGAAGTAAATCTTAAGCATGTATGAATATTGAGAGT 132
                                                                                                                                              Score 48; DB 18; Length 16
Pred. No. 0.31;
0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 GEGTACATGTGTACACATTCTGAACATGTGTGTATATTGAAAAT 754
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Larity 49.4%; Pred. No. 9;
Conservative 0; Mismatches 155; Indels
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 256988
LENGTH: 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                            Query Match 6.2%;
Best Local Similarity 46.2%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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) LOCATION: (379615)
US-10-312-841-2
                                                                                      ; ORGANISM: Human
US-10-027-632-256988
                                                            TYPE: DNA
ORGANISM: Human
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LENGTH: 3673778
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Best Local Simi
Matches 153;
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TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATATTTTAAAAAGGATCGTTTTTGCCATGTATAAATTTTTCAAACATTAACTTTCAGGG
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US-10-433-793-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-714A-65
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PUDICACION NO. US20040048254A1

FRENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Lumor Suppressor genes and oncogenes
TITLE OF INVENTION: Lumor Suppressor genes and oncogenes
FILE REPERENCE: 5013.106
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT PILING DATE: 2003-01-21
FRIOR APPLICATION NUMBER: DE 10013847.0
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR APPLICATION NUMBER: DE 10019058.8
FRIOR PILING DATE: 2000-04-06
FRIOR PILING DATE: 2000-04-07
FRIOR PILING DATE: 2000-04-07
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CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 36
LENGTH: 33053
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Publication No. US20040142334A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-433-793-36
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APPLICANT: Epigenomics AG TITLE Diagnose von bedeutenden genetischen Parametern innerhalb des MHC TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC FILE REFERENGE: BO1/1208/WO CURRENT APPLICATION NUMBER: US/10/312,841 CURRENT FILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 2 SEQ ID NO 1
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                                                                                                                                                                                             14921 TTTATGATTATTTTTTTTTAGTATAAGTATTATAAAGAGATTAGTTTTGTTTTATAGG 14980
                                                                                                                                                                                                                                                                           15041 TÄTACGTTTTGTTGTGAAGGTTGTGGTGTTTTTTGTGÄTTTTATTAAGAATGTTTTTTGG 15100
                                                                                                                                                                                                                                                                                                                                                       15101 TTGATGİTTİRĞİAAALĞIAGİGĞIGTATTATİĞITĞAATAİAİTTATATİAİTTTİT 15160
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                                                                              290 TTAATAACCATGTGTCATCTAGAATGAAGTTATATTTTAAAAAGGATCGTTTTTTGCCATG
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Length 33053;
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    DB 20;
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Best Local Similarity 46.7%; Pred. No. 20;
Matches 148; Conservative 0; Mismatches 169;
  Score 46.6; DB 20;
Pred. No. 2.6;
0; Mismatches 169;
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  6.0%;
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                                       Conservative
                  Similarity
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; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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                      Best Local Sim
Matches 148;
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Search completed: November 8, 2005, 23:53:38 Job time : 1012.4 secs

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 376)

1 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Share,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-KT0005-
151100-001-b03&t3=2000-11-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 376.
Lication/Qualifiers
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/note="Organ: bladder_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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AUTHORS
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KEYWORDS
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AU234451 AU234451
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AL064109 Drosophil
AL06890 Brosophil
AL106896 Brosophil
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9bb_est2:

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EST 10-JAN-2001 mRNA sequence.

PUJDS79TB OG1EB38TV

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Drosophil

Tetraodon

ALL106190 CK657214 CK657214 ALL175696 AL065414 BZ666860 AL065114 BZ696860 AL101513 AL0778356 AL064091 AL064091 AL064091 AL064091 AL064091 AL064091 AL064091 AL064093 AL06893 BZ687506 CG209274 CG15113 CG15113 CG15113 CG209274 CG15113 CG209274 CG209274 CG209274 CG209274 CG209274 CG209274 CG209274 CG209274 CG209274 CG209274

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Drosophil PUBHR65TD OG1EB38TH P048-1-C0 rc24b11.y

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University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewinGuiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pleter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBAC) by viniversity of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG2202-34480-11828
from USBA-CSRESs and AG99-35205-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
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Larkin,D.M., Everts.van der Wind,A., Rebeiz,M., Schweitzer,P.,
Larkin,D.M., Everts.van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S. Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J. and Lewin,H.A.
Bovine BAC end sequences from CHORI-240 library
Unpublished (2003)
Other GSSs: CH240 95D2.TJ
Contact: Harris Lewin
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                                                                                                                                                                                                                                                                                                                            1 TCATGTAGGTAAGACTGTGTAGAATGTCGGGTCTCGATGTTGGCGCTATTCAAGCCCTGA 60
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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/clone lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1;
/note="Vector: pTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1;
/lote=ford bull il Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pleter de Jong"
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Best Local Similarity 95.8%; Pred. No. 8.4e-14;
Matches 115; Conservative 0; Mismatches 4; Indels 1
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/strain="breed: Hereford"
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clone="CH240_95D2"
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Class: BAC ends.
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AU234451
AU234451 Bovine placenta cDNA Bos taurus cDNA clone Cln1153 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 CAATAGAAAGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATG 719
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 390)
Obna, H., Lejukole, H.Y., Taniguchi, Y., Yamada, T., Akagi, S.,
Yasue, H. and Sasaki, Y.
Analysis of expressed sequence tags from a cDNA library of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 CTTTAGGTTAGCAGGCATGTGCCTCTAGAACAAGCTTGTATTTTCATAAATGTCTT
                                                                                283 CTTAGGCTTAATAACCATGTGTCATCTAGAATGAAGTTATATTTTAAAAAGGATCGTTTT
                                         Gарв
                                         3;
8.2%; Score 63.4; DB 9; Length 358; larity 71.5%; Pred. No. 0.00014; Conservative 0; Mismatches 36; Indels
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69.1%; Pred. No. 0.00025;
ive 0; Mismatches 36; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kyoto University
Sakyoku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6323
Fax: 81-75-753-6340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tyamada@jkans.jkans.kais.kyoto-u.ac.j
This clone was obtained from a 3' end cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="Cl11153"
/tissue type="placenta"
/clone_Tlb="Bovine placenta cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Takahisa Yamada
Graduate School of Agriculture
                                                                                                                                                                                                                                        400 AGTTTTTTTTAAGTCTG 416
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                                                                                                                                                                                                                                                                             AGTTTTTTTAAGTCTG 4
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Bos taurus
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Best Local Similarity
Matches 98; Conserv
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Matches 123; Conserv
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collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster agenome using these BACe. For further information please see http://www.fruitily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial BCoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 TAGAATGAAGTTATATTTTAAAAGGATCGTTTTTGCCATGTATAAATTTTTCAAACATTA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAGGAAAGTAGGTGAAGTGATTTTAATAGATGTTTCTTTTATGAAATAATTTTTAAAA 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 AGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGTGTACACAT 728
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BACR12P23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 7.5%; Score 58.2; DB 9; Length 1 Il Similarity 14.3%; Pred. No. 0.0031; 66; Conservative 223; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           729 TCTGAACATGTGTATATTGAAAATCTTGTCTTTTTTA 769
                                                                                                                                                                                                                                                                                                             1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROBK10"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="RPCI-98"
/note="end : TBT3"
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GSS.
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Best Local Similarity 14.3%;
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CNS005RL/c
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                            AUZ/BB52 400 bp mRNA linear EST 02-JUL-2002
AUZ/BB52 Cloned bovine placenta CDNA Bos taurus CDNA clone
placentall53 3', mRNA sequence.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACROSKIO of RPCI-98 library from Drosophila melanogaster (fruit
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Direct Submission
Submitsed (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
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                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                          1 (bases 1 to 400)
Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and
Sasaki,Y.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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.larity 69.1%; Pred. No. 0.00025;
Conservative 0; Mismatches 36; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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/clone="placenta1153"
/dev stage="60 embryonic day"
/clone_lib="Cloned bovine placenta cDNA"
                                                                                                                                                                                                                                                                                                                                   EST analysis of cloned bovine fetus and placenta Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: oishi@jkans.jkans.kais.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
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Drosophila melanogaster
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Graduate School of Agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fly), genomic survey sequence.
AL063921
AL063921.1 GI:4941778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-75-753-6331
Fax: 81-75-753-6340
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GSS 03-JUN-1999

REFERENCE AUTHORS TITLE

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Web: www.genoscope.cns.fr)

Web: www.genoscope.cns.fr)

Determination of this BAC-and sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT.98 and was constructed by partial BCORI disection of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed describtion of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 TTAATAACCATGTGTCATCTAGAATGAAGTTATATTTTAAAAAGGATCGTTTTTGCCATG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 AAGTCTGTGCAGTAATAGAGGTATCGTCATTCATGTGACATAAAAGATGGAAAGGGGCTT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 TITATATTAATWAWATTAATAWATTAATATAWATTWITWIAAATWTAATWWATTAATWWATTAATWATTAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGAAATAATTTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTG-- 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 ТАМММААТИАМТТАТТТААТААМТААТТАААТТАТТАААДАТТТТТАТИАААААТАТТТТ 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 CAGAATGAAATCCAATAGAGAAGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAG 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 TGGTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGCTCAGGGAAAGCAAT
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                                                                                                                           Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                       Drosophila melanogaster (fruit fly)
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/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                         Drosophila melanogaster
AL069706.1 GI:4949849
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                                                                                                                                           Direct submitted (02-UUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be toomed at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACKS9823 of RPCI-98 library from Drosophila melanogaster (fruit AL069706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 TCAAACATTAACTTTCAGGGTTATTAATCCTTTTAAGGTCTAGTTTTTCTTAAGTCTGTG 418
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="BACR12F23"
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/note="end : T7"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416
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809 GKKKKKKAAAKKKAADRTKKTKWDAAAAAAKKTKDKGKKKKKTKKKTTKKKKKKKKK 868
                                                              672 TAAATITATITIGGGCATGTACATITIGGCAGCCTAGGCTGTGTACATGTGTACACATICT 731
                                                                                                                                                   929 GKKKKGGKKGKKGKKKTKKTKKKKKKKKADAAKGKTKKRAAAADAAAADWTDAATKKK 988
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                                        512 ATAGAAAGCATTGTAGGCTCAGGGAAAGCAAACATTCAGAATGAAATCCAATAGAGAAGG
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                             /organism="Drosophila melanogaster"
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/plasmId="pBeloBAC11"
/note="end : T7"
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                   Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACKA8B19 of RPCI-98 library from Drosophila melanogaster (fruit
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AL078714.1 GI:5102004
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Matches 91: Concount.
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|mol_type="genomic DNA"
|db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
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/clone_lib="RPCI-98"
/note="end : TET3"
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Ali76843.1 GI:7814900
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Acanthomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
531 ATGAAATAATTITTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTGTGG 590
                           452 AAAGATGGAAAGGGGCTTCATTTATTAGTGATGGAAATAGGAAAGTAGGTGAAGTGAT 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/mol_type="genomic DNA"
/db xrefe="texon:99883"
/clone="125004"
/clone lib="G"
/note="Genoscope sequence ID : COAG225BH02LP1~end : T7"
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Tetraodon nigroviridis genome survey sequence T7 end of clone
225004 of library G from Tetraodon nigroviridis, genomic survey
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Bilthaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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AL106578
Geo.
                      537 TAATTTTAAAAGATTGTCCAGCCCTGCATGATTTATGATGAATCATTTTGTGGTCTGTT
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Ephydroidaa; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
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574
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                                                                                                                   514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2),
149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 TCGTTTTTGCCATGTATAAATTTTCAAACATTAACTTTCAGGGTTATTAATCCTTTTAAG 395
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Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (Dases 1 to 500)

Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.

FULL-malaria: a database for a full-length enriched cDNA lib

from human malaria parasite, Plasmodium falciparum

Nucleic Acids Res. 29 (1), 70-71 (2001)
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Pred. No. 0.1;
0; Mismatches 149; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="XPFn7173"
/dev_stage="erythrocytic stage"
/clone_lib="Sugano Malaria cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .500
/organism="Plasmodium falciparum 3D7"
/mol type="mRNA"
/isoTate="3D7"
                                                                                                                                                                                                                                                                               575 ATGAATCATTTTGTGGTCTGTTAGTTACTTTTAGAGAAT 613
                                                                                                                                                                                                                                                                                                                       1218 TİTATAGATAİTTİTAİATİTATİTATAİTİTTAT
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Fax: 81-3-5449-5410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.19
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S Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission

Direct Submission

Submitted (17-NOV-2003) Magahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Subhiro-chou,Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriegsc.riken.jp, UKL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9199

e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                   AG382019 1530 bp DNA linear GSS 03-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-192818.T7, genomic survey
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                                       335 ATCGTTTTGCCATGTATAAATTTTCAAACATTAACTTTCAGGGTTATTAATCCTTTTAA 394
                     631
                                                                                            741 AARAARAAAAATT----ATTKRRKBKRRKKKRRKKKRAAAAKKKBRKKTGRKGRRKG 796
                                                                                                                                                                                                 692 CATTITIGGCAGCCTAGGCTGTACATGTGTACACATTCTGAACATGTGTGTATATTGAA 751
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                  ATGATGAATCATTTTGTGGTCTGTTAGTTACTTTTAGAGAATAGAAAGCATTGTAGGCTC
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BAC end Sequences of Library MSMg01
Unpublished
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/clone lib="MSMg01 Mouse Male BAC Library"
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/sub_species="molossinus"
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/clone="MSMg01-192E18.T7"
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957 KKKKKKKKKKKTTTTTTTR 880
                                                                                                                                                                                                                                                          752 AATCTTGTCTCTTTTTTTGTTA 775
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Mus musculus molossinus
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LIBRARY
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1002 TTTTKKDKRAAARTTTTTGRDGAKARAATKKKTTTGTGTAKTGGGTGKKKRKGKDAA 1061
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                    ATAGAGAAGGTAAATTTATTTGGGCATGTACATTTTGGCAGCCTAGGCTGTGTACATGTG 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lax scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Benock, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome-wide analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="101H21"
/clone lib="G"
/note="Genoscope sequence ID : COBGIOICDIILP1-end : T7"
                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis genome Burvey sequence T7 end of clone
101H21 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of freshwater Dufferfish Tetraodon nigroviridis
                                                                                                                                                      6.6%; Score 51.4; DB 9; 39.5%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Mismatches 180;
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Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                  945 bp
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AL285149.1 GI:8023560
GSS; genome survey sequence.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISCO8 of DrosBAC library from Drosophila melanogaster (fruit ALIO6552
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                     AAGAATRGGDGMRAGTGTTTBTKTTTTGWWAAMAWAAAAAWADARWWADATTTTWTTAW 761
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Bukaryota; Metaroa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="end : SP6"
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Result

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AP012873 308 bp DNA linear PRI 03-MAY-1999
Homo sapiens PPARG gene, isoform 1, promoter and 5'UTR sequence.
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'note="peroxisome proliferative activated receptor, gamma"
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AC126054 Mus muscu
AC021226 Homo sapi
AC021256 Homo sapi
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AC100483 Mus muscu
AC023563 Homo sapi
AC102856 Homo sapi
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Fajas,L., Auwerx,J., Saladin,R. and Briggs,M.
Direct Submission
Submitted (07-JUL-1997) Cardiovascular Res., Ligand
Pharmaceuticals, 9393 Towne Centre Dr., San Diego, CA 92121-3016, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Biol. Chem. 272 (30), 18779-18789 (1997)
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Fajas, L., Auboeuf, D., Raspe, E., Schoonjans, K., Lefebvre, A.-M.,
Saladin, R., Najib, J., Laville, M., Fruchart, J.-C., Deeb, S.,
Puig-Vidal, A., Flier, J., Briggs, M., Vidal, H., Staels, B. and

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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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Bao, W., Bao, J., Bao, Q., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H.,

Bao, W., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C.,

Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y.,

Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, O., Qi, x., Song, L.,

Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J.,

Wang, J., Wang, J., Wang, L., Wang, R., Wang, X.,

Wang, Y., Wu, D., Wu, Q., Xie, Zhang, H., Zhang, H., Zhang, L., Zhang, L., Zhang, L., Zhang, L., Zhang, L., Zhang, Z., Zhang, Z., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Z
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Genetics, Chinese Academy v. 100101, P.R.China
On Nov 8, 2002 this sequence version replaced gi:15148930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 135675;
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Homo sapiens chromosome 3 clone RP11-33519 map 3p,
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Pred. No. 5.7e-09;
0; Mismatches 4
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                           Center: Beijing Center
Center code: Beijing
Website: http://hgc.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgc@lgtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="3p"
/clone="RP11-167M22"
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AC091492.2 GI:24796732
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Best Local Similarity 96.8
Matches 121; Conservative
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1 (Dases 1 to 1356/75)

8 Wu,Q., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Li,C., Li,C., Li,C., Li,F., Li,F., Li,G., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L., Li,L.,
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Submitted (13-AUG-2001) Human Genomic Center, Institute of Genetics.

Chinese Academy of Sciences, Datun Road, Beijing, Beijing Genetics. Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

By Abao, Bao, W., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, C., Li, W., Li, W., Li, W., Tan, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Li, Y., Liu, N., Liu, Li, Li, Y., Liu, Y., Liu, N., Liu, B., Li, Y., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, N., Liu, B., Liu, Rang, L., Zhang, M., Zhang, M., Zhang, M., Zhang, M., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhan
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Unpublished
E 2 (bases 1 to 135675)
S Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
S Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
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Li,G., Li,J., Li,L., Li,S., Li,T., Li,Y., Li,U.,Y., Li,U.,Y.,
Li,W., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tao,R., Wang,Y.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,Y.,
Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B.,
Zhang,X., Zhang,X., Zhang,H., Zhang,L., Zhang,L., Zhang,Y.,
Yu,J. and Yang,H.,
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Homo sapiens chromosome 3 clone RP11-167M22 map 3p, complete
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Direct Submission
Submitted (08-NOV-2002) Human Genomic Center, Institute of
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         Length 308;
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         100.0%; Score 125; DB 9;
100.0%; Pred. No. 7.4e-09;
ive 0; Mismatches 0;
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Query Match 100.
Best Local Similarity 100.
Matches 125; Conservative
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1. .180963
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/clone="RP11-335I9"
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Direct Submission

Submitted (26-APR-2001) Human Genomic Center, Institute of Genetics, Chinase Academy of Sciences, Datum Road, Beijing, Beijing 100101, PR. China

S Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Bao, J., Bao, Q., Bao, W., Bian, X., Gong, J., Gan, Q., Gux, G., Gu, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, C., Li, Y., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., W., M., W., W., W., Wang, H., Wang, J., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Wang, L., Zhang, H., Zhang, H., Zhang, H., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, H., Zhang, L., Zhang, M., Zhang, H., Zhang, L., Zhang, M., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Direct Submission

M. Submitted (08-NOV-2002) Human Genomic Center, Institute of Genetics Chinnes Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R. China

Sabo, W., Bao, J., Beo, Q., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., W., Guo, D., Guo, Z., Li, G., Li, L., Li, S., Li, T., Liu, Y., Liu, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Sun, W., Tan, X., Tao, R., Wang, Y., Wang, Y., Wang, Y., Wang, Y., Wang, Y., Wang, Y., Wang, Y., Zhang, R., Wang, R., Wang, Y., Wang, Y., Zhang, R., Wang, R., Wang, Y., Wang, Y., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, R., Zhang, 
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                                                                               Dao, W., Bao, J., Bao, Q., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Pan, H., Feng, X., Gong, J., Guan, Q., Gu, C., Guo, Z., Guo, Z., Hei, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, M., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Li, W., Liu, B., Wang, J., Wang, L., Wang, X., Wang, X., Wang, X., Wang, Y., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, Z., Zhu, B., Zhu, N.,
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator: ET 55% of reads
Assembly program: Phrap, version 0.990129
Consensus quality: 369 bases at least Q40
Consensus quality: 755 bases at least Q20
Insert size: 773; sum-of-contigs
Quality coverage: 1.48x in Q20 bases;sum-of-contigs
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http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
Center:hgc@igtp.ac.cn
Center project name:1% project
Center clone name: RP11-33519
Yu,J. and Yang,H.
Chromosome 3p genomic sequence
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Center code:Beijing
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PRI 16-JUN-2004
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1 (Bases I to 148828)
Rieder, M.J., da Ponte, S.H., Kuldanek, S.A., Rajkumar, N., Smith, J.D., Toth, E.J. and Nickerson, D.A.
Direct Submission
Submitted (30-SEP-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
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Direct Submission

Submitted (16-UTN-2004) Genome Sciences, University of Washington, 1705 NB Pacific, Seattle, WA 98195, USA

Sequence update by submitter

On Jun 16, 2004 this sequence version replaced gi:23953882.

To cite this work please use: SeattleSNPs. NHLBI Program for Genomic Applications, UW-FHCRC, Seattle, WA

(URL:http://pga.mbt.weshington.edu).
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Homo sapiens peroxisome proliferative activated receptor gamma VPPARO, gene, complete cds.
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Score 118.6; DB 9; Length 180963;
Pred. No. 5.1e-09;
0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL356736 108399 bp DNA linear HTG 13-JUN-2001
Homo gapiens chromosome 1 clone RP11-422P10, 26 unordered pieces.
                                                                                                                                                                                                                                                                            1922 CCCCGGCCCCGGCCCCCGCCCCCCACCCCCACCCCCACCCCCAGCCGGCGCGCGCGC 1981
                                                                                                                                                                                                                                                                                                                                                1982 GCCGCCCCGCGGCCGGGCCCGGCCCGACCCGGCTCCGCCGCGGGGCAGCGGGGGC 2041
                                                                                                                                                                                                                                                                                                                            61 GCCCGCCCCCGCGCCCGGGCCCGGCCCCGACCCCGGTTCCGCCGCGGGCAGCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9213961.
                                                                                                                                                                                                                                                    1 CCCTGCCCTGCCCCTGCCCCCACCCCCACCCCCACCCCCACCCCCAGCCGGCGCCCGC
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5 Sequencing vector: TAPA; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 95168 bases at least Q40 Consensus quality: 107890 bases at least Q20 Insert size: 105899; sum-of-contigs Insert size: 15533; 8.5% error; agazone-fp Quality coverage: 2.72x in Q20 bases; sum-of-contigs Quality coverage: 2.72x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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0
                                                                                                                                                                                Length 148828;
                                                                                                                                                                            93.6%; Score 117; DB 9; Length 14
96.0%; Pred. No. 9.2e-09;
ive 0; Mismatches 5; Indels
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/rpt_type=dispersed
22582. 22916
/rpt_family="MER1_type"
/rpt_type=dispersed
22917. 23104
/rpt_family="L2"
/rpt_family="L2"
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
22493. .22581
                                                                                                                                                                            Query Match
Best Local Similarity 96.0
Matches 120; Conservative
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repeat_region
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VERSION
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SOURCE
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AUTHORS
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AL356736
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BX936377 238794 bp DNA linear HTG 10-FEB-2004
Danio rerio clone DKEY-149J2, *** SEQUENCING IN PROGRESS ***, 14
                                                                                                                                                                                                                                                                                                                             Submitted (09-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, cambridgeshire, CB10 15A, UK. E-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 10, 2004 this sequence version replaced g1:42491169.
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 2131615 bases at least Q40
Consensus quality: 213776 bases at least Q30
Consensus quality: 234285 bases at least Q30
Insert size: 237494; sum-of-contigs
Insert size: 196119; 7.4% error; agarose-fp
Quality coverage: 8.08x in Q20 bases; sum-of-contigs Quality
coverage: 9.83x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently consists of lt contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
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of 34772 bp in length
100 bp
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Center: Wellcome Trust Sanger Institute
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contig
gap of
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HTG; HTGS PHASE1.
Danio rerIo (zebrafish)
Danio rerio
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30743:
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230987:
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BX936377
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 2182 GCGGC 2186
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179162
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                                                  RESULT 6
BX936377/c
LOCUS
                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                    DEFINITION
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AUTHORS
TITLE
JOURNAL
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Ja575. 44658

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fragment_chain:3"
4759. 49335

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60589. 57658
60589. 67658
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69888. 77142
/notes assembly_fragment:00679
fragment_chain:6"
/7243. 81918
/notes assembly_fragment:00766
fragment_chain:6"
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12019. .86773
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note="assembly_fragment:00571"
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3297. .25747
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ragment chain:1"
5848. .28603
                                                                /note="assembly_fragment:00087
fragment_chain:2"
28704. .33157
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Best Local Similarity 68.0°
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   misc_feature
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E. C. (Dases 1 to 11574).

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzklugh, W., Porrest, C., Punke, R., Gage, D., Horton, L., Howland, J., Grandyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Melfrim, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                            HTG 12-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                        AC012300 171574 bp DNA linear Homo sapiens chromosome 17 clone RP11-248L3 map 17, IN PROGRESS ***, 48 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-------- Project_Information
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of 1099 bp in length
100 bp
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of 1079 bp in length
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of 1039 bp in length
                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-248L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L670
Center clone name: 248_L_3
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9543:
9643:
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Homo sapiens (human)
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                                                                                                                                                                                                             Homo sapiens
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AC012300
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DEFINITION
                                                                                                                               ACCESSION
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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AUTHORS
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235549: contig of 4562 bp in length 235649: gap of 100 bp 238794: contig of 3145 bp in length.
                                                                                                                                                                                                                                                                                           /notes assembly fragment:00031
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30744._.33315
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* 146970: contig of 7223 bp in length
* 146971: contig of 7223 bp in length
* 147071: 147070: gap of 100 bp
* 147071: 156784: contig of 9714 bp in length
156785: 156884: gap of 100 bp
156885: 171574: contig of 14690 bp in length.
Location/Qualiflers
1. .171574: contig of 14690 bp in length.
| command type="genomic DNA" | color: command type="genomic DNA" | color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: color: 
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1. 1038
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Isubmitted (07-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:7107923.

All repeats were identified using RepeatWasker:
Shit, A.F. A. & Green, P. (1996-1997)
                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135119)
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                               ACO11578 135119 bp DNA linear HTG :
Homo sapiens clone RP11-12P9, LOW-PASS SEQUENCE SAMPLING
AC011578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Unpublished
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 53121)

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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens chromosome 17, clone RP11-1230B22
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* NOTE: This record contains 66 individual
* sequencing reads that have not been assembled into
contiggs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-fifth and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
* be preserved.
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Mus musculus clone RP23-467G14, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 68330)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, Cone RP23-467G14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 85 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            647: contig of 647 bp in length
747: gap of 100 bp
1422: contig of 675 bp in length
1522: gap of 100 bp
2229: contig of 707 bp in length
3309: gap of 100 bp
3101: contig of 672 bp in length
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Mus musculus (house mouse)
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                                                                 AC112672 72645 bp DNA linear HTG 09-MAY-2002
Mus musculus clone RP24-418P12, LOW-PASS SEQUENCE SAMPLING.
AC112672
                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MXY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAY 9, 2002 this sequence version replaced gi:18860694. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-418P12
Unpublished
                                                                                                                                                             HTG; HTGS PHASE0.
Mus musculus (house mouse)
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                     * NOTE: This record contains 89 individual

* Gequencing reads that have not been assembled into

* contigg. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.
                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: project Information
Center project name: L21384
Center clone name: 418_P_12
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                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 80542)

Birren, B., Linton, L., Nusbaum, C. and Lander, B.

Homo sapiens, clone RP11-30L16
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Blaten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bladwin, J., Barna, N., Beckerly, R., Bogulavky, L., Boukhgalter, B., Brown, A., Castle, A., Colanglo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreita, P., FizzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Mones, C., Kann, L., Karates, A., Horton, L., McBwan, P., McGurk, A., McKernan, K., McGonald, P., Marquis, N., McKernan, K., McGonald, P., Marquis, N., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 84701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-1070-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6456192. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatWasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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contig of 886 bp in length
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gap of 100 bp
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Unpublished
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Homo sapiens (human)
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Homo gapiens clone RP11-28B3, LOW-PASS SEQUENCE SAMPLING.
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g of 774 bp in length
f 100 bp
g of 768 bp in length
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g of 688 bp in length
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f 100 bp
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of 762 bp in length
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GAG Bioscience GmbH (DE)
Location/Qualifiers
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Dna markers for cattle or beef produc
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/wol_type="unassigned DNA"
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/noTe="Rind (SNP-Marker)"
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